

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 23, 2003, 12:00:30 ; Search time 1477 Seconds  
(without alignments)  
276.978 Million cell updates/sec

Title: US-09-745-763-36\_COPY\_231\_240  
Perfect score: 10  
Sequence: 1 TACTCTEDAA 10

Scoring table: OLIGO  
Xgapop 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2688711 seqs, 20454813386 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5764739

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlp  
-Q=/cgr2\_1/USPTO.epool\_p/US09745763/runat\_23122003\_120023\_20083/app.query.fasta-1.199  
-DB=GenEmbl -OPMT=faastap -SUFFIX=olip2n.rge -MIMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNTS-bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALLGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTMT=ptco  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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1: gb\_Da.\*  
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3: gb\_In.\*  
4: gb\_Om.\*  
5: gb\_Ov.\*  
6: gb\_Pat.\*  
7: gb\_Ph.\*  
8: gb\_Pl.\*  
9: gb\_Pr.\*  
10: gb\_Ro.\*  
11: gb\_Sts.\*  
12: gb\_Sy.\*  
13: gb\_Un.\*  
14: gb\_Vi.\*  
15: em\_Ba.\*  
16: em\_Fun.\*  
17: em\_Hum.\*  
18: em\_In.\*  
19: em\_Mu.\*  
20: em\_Om.\*  
21: em\_Or.\*  
22: em\_Ov.\*  
23: em\_Pat.\*  
24: em\_Ph.\*  
25: em\_Pl.\*  
26: em\_Ro.\*  
27: em\_Sts.\*  
28: em\_Un.\*

29: em\_Vi.\*  
30: em\_Htg\_Hum.\*  
31: em\_Htg\_Inv.\*  
32: em\_Htg\_Other.\*  
33: em\_Htg\_Mus.\*  
34: em\_Htg\_Pin.\*  
35: em\_Htg\_Rod.\*  
36: em\_Htg\_Mam.\*  
37: em\_Htg\_Vrt.\*  
38: em\_Sy.\*  
39: em\_Htg\_Hum.\*  
40: em\_Htg\_Mus.\*  
41: em\_Htg\_Other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	100.0	1472	9 AF107834	AF107834 Homo sapi
2	100.0	100.0	1596	10 AF107835	AF107835 Mus muscu
3	100.0	100.0	1716	10 AF009513	AF009513 Mus muscu
4	100.0	100.0	1778	6 BD105816	BD105816 Secretary
5	100.0	100.0	1794	9 AF119386	AF119386 Homo sapi
6	100.0	100.0	1796	10 BC037067	BC037067 Mus muscu
7	100.0	100.0	1851	6 BD106411	BD106411 Secretary
8	100.0	100.0	1860	6 AX006440	AX006440 Sequence
9	100.0	100.0	1860	6 BD127520	BD127520 Primer fo
10	100.0	100.0	1928	9 AK075132	AK075132 Homo sapi
11	100.0	100.0	1928	9 BC020689	BC020689 Homo sapi
12	100.0	100.0	144703	9 AP003112	AP003112 Homo sapi
13	100.0	100.0	157927	9 AP006278	AP006278 Homo sapi
14	100.0	100.0	203469	2 AC123654	AC123654 Mus muscu
15	100.0	100.0	214287	2 AC129951	AC129951 Mus muscu
16	70.0	70.0	819	11 BV035880	BV035880 S12P6043
17	70.0	70.0	2000	6 AK655910	AK655910 Sequence
18	70.0	70.0	4560	1 AF060183	AF060183 Mycobacte
19	70.0	70.0	25851	1 AF125999	AF125999 Mycobacte
20	70.0	70.0	27516	1 AY130970	AY130970 Mycobacte
21	70.0	70.0	71286	1 AF143772	AF143772 Mycobacte
22	70.0	70.0	93098	5 AL591389	AL591389 Zebrafish
23	70.0	70.0	99427	2 AP003821	AP003821 Oryza sat
24	70.0	70.0	112182	2 AC141177	AC141177 Rattus no
25	70.0	70.0	131033	5 AL591370	AL591370 Zebrafish
26	70.0	70.0	141707	8 AP005182	AP005182 Oryza sat
27	70.0	70.0	154152	5 AL953886	AL953886 Zebrafish
28	70.0	70.0	157797	8 AP005184	AP005184 Oryza sat
29	70.0	70.0	161370	9 AC093800	AC093800 Homo sapi
30	70.0	70.0	163291	2 AC102390	AC102390 Mus muscu
31	70.0	70.0	173395	2 AP006061	AP006061 Oryza sat
32	70.0	70.0	181773	10 AC087336	AC087336 Mus muscu
33	70.0	70.0	190807	2 AC116586	AC116586 Mus muscu
34	70.0	70.0	199986	10 AC090563	AC090563 Mus muscu
35	70.0	70.0	209143	2 AC134810	AC134810 Rattus no
36	70.0	70.0	212404	10 AC090127	AC090127 Mus muscu
37	70.0	70.0	213347	2 AL831741	AL831741 Mouse DNA
38	70.0	70.0	225054	2 AC101693	AC101693 Mus muscu
39	70.0	70.0	226464	2 AC099442	AC099442 Rattus no
40	70.0	70.0	264110	2 AC122626	AC122626 Rattus no
41	70.0	70.0	270297	2 AC126661	AC126661 Rattus no
42	60.0	60.0	22	6 BD131707	BD131707 Eucaryoti
43	60.0	60.0	239	9 HSA509104	AB0509104 Homo sapi
44	60.0	60.0	240	9 AB067802S4	AB067805 Homo sapi
45	60.0	60.0	256	10 QRT5	AF090335 Mus muscu

RESULT 1

## ALIGNMENTS

AF107834 1472 bp mRNA linear PRI 12-JUL-1999  
 LOCUS AF107834 Homo sapiens clone LCH1 aminopeptidase mRNA, complete cds.  
 DEFINITION AF107834  
 ACCESSION AF107834  
 VERSION AF107834.1 GI:5442029  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 1472)  
 AUTHORS Liu, C.H., Lin, B.Y., and Chang, L.Y.  
 TITLE Cloning of the human aminopeptidase gene  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1472)  
 AUTHORS Liu, C.H., Lin, B.Y., and Chang, L.Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-NOV-1998) Institute of Biomedical Sciences, Academia Sinica, RM 433, 128, Yen-Chiun-Yuan Road SEC 2, Taipei 11529, Taiwan  
 FEATURES  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="LCH1"  
 /tissue\_type="liver"  
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 54.1472  
 /note="secretory protein"  
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 /product="aminopeptidase"  
 /protein\_id="A043214.1"  
 /db\_xref="GI:5442030"  
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 VHLPEPRIPMERGESAVMLEPRHKMIIILGSSIGTPPEGITAEVLVTSFDELQ  
 RASEARCKIIVYNQPYTEKTVQYRGVAAKVAASLIQSVASFSYSPHTG  
 IOEYODGVPKIPITACITVEDAMSMRMSRGNKIIVHLEMGAKTIPDTSFNTVAITGS  
 GSKYPEQVIVSGHLSMDVGGALDDGGGAFISMEALSLKDLGRPKRTLRLVLT  
 AEQGGVGAFOYQDLHKVNISYSLVMSDGLTLPGLQPTGSEKAAINAEVMSLL  
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 AAAYVAAYVAVDDEMLPRS"

BASE COUNT 411 a 325 c 381 g 355 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 0.0103 Length: 1472  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AF107834 (1-1472)  
 Oy 1 ThzAlaCyseIleThrValGluAspAlaGlu 10  
 Db 744 ACAGCCTGTATTACGTCGGAAGACGACGAA 773

RESULT 2  
 LOCUS AF107835 1596 bp mRNA linear ROD 12-JUL-1999  
 DEFINITION AF107835 Mus musculus clone LCH-M1 aminopeptidase mRNA, complete cds.  
 ACCESSION AF107835  
 VERSION AF107835.1 GI:5442031  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1596)  
 AUTHORS Liu, C.H., Lin, B.Y., and Chang, L.Y.  
 TITLE Cloning of the mouse aminopeptidase gene

JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1596)  
 AUTHORS Liu, C.H., Lin, B.Y., and Chang, L.Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-NOV-1998) Institute of Biomedical Sciences, Academia Sinica, RM 433, 128, Yen-Chiun-Yuan Road SEC 2, Taipei 11529, Taiwan  
 FEATURES  
 source  
 1.1596  
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 184.1596  
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 ASEARCKIIVYNQPYTEKTVQYRGVAAKVAASLIQSVASFSYSPHTG  
 KYODGVPKIPITACITVEDAMSMRMSRGNKIIVHLEMGAKTIPDTSFNTVAITGS  
 MYPEEVVIVSGHLSMDVGGALDDGGGAFISMEALSLKDLGRPKRTLRLVLTAE  
 ECGIGASQYVEELHKVNISKYSLVMSDGLTLPGLQPTGSEKAAINAEVMSLL  
 LNTKVPFSNBEQDINFWIQAGVPGASLDDLYKFFFHSHSGDTMTVMDPKQNVV  
 AAAYVAAYVAVDDEMLPRS"

BASE COUNT 415 a 357 c 421 g 403 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 0.011 Length: 1596  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AF107835 (1-1596)  
 Oy 1 ThzAlaCyseIleThrValGluAspAlaGlu 10  
 Db 868 ACAGCCTGTATTACGTCGGAAGACGACGAA 897

RESULT 3  
 LOCUS AF009513 1716 bp mRNA linear ROD 01-JUN-1998  
 DEFINITION AF009513 Mus musculus hematopoietic lineage switch 2 (HLS2) mRNA, complete cds.  
 ACCESSION AF009513  
 VERSION AF009513.1 GI:3169728  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1716)  
 AUTHORS Williams, J.H., Chan, C.-Y., and Klinken, S.P.  
 TITLE Hematopoietic lineage switch 2 (HLS2), a novel mRNA species induced during an erythroid to myeloid lineage switch  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1716)  
 AUTHORS Williams, J.H., Chan, C.-Y., and Klinken, S.P.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-JUN-1997) Biochemistry Department (Laboratory of Cancer Medicine), University of Western Australia, Royal Perth Hospital, Wellington Street, Perth, WA 6001, Australia  
 FEATURES  
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 1.1716  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"

gene 1. .1716  
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CDS 97. .1398  
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/product="hematopoietic lineage switch 2"  
/protein\_id="AAC17945.1"  
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AKAILNLAAYGKQNSYERLGLVDTVGRRLSGSKLEKATIMQNLQDGLBNVH  
LEQVRIPIHMERGESAVMLEPRILKVALILGLSSIGPPGKITAEVLVVASFDLQR  
ASEARGKILVYNQPTGYEKTQVRYGAVAAKVGAVASLIQSVASFSIYSHTGIQ  
KYODGVPKIPACTIVEDAMEMSRMASRGNKIYIHLMEGAKTVPDTSFNTVAITGS  
MYPDYOGALDDGGAGFISWEALSLYKDLGRPLRLVLTAEBOGGIGASOYBE  
LHKANISKYSLWMEADSGTFLPGIOFTSGDKARAIKREYMNLLQPLNTKVRNSNEG  
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BASE COUNT 476 a 370 c 414 g 456 t

ORIGIN

Alignment Scores:  
Pred. No.: 0.0117 Length: 1716  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AF009513 (1-1716)

Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
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781 ACAGCCTGATTACGTTGAAGATGCAGAA 810

Db

RESULT 4  
BD105816  
LOCUS BD105816  
DEFINITION Secretory protein.  
ACCESSION BD105816  
VERSION BD105816.1 GI:23200634  
KEYWORDS JP 2002502234-A/7.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 1778)  
AUTHORS Jacobs,K., McCoy,J.M., Racie,L.A., Lavallie,E.R., Merberg,D. and Spaulding,V.  
TITLE Secretory protein  
JOURNAL Patent: JP 2002502234-A 7 22-JAN-2002;  
GENETICS INSTITUTE INC  
COMMENT PN JP 2002502234-A/7  
PD 22-JAN-2002  
PF 16-APR-1997 JP 1997537384  
PR 18-APR-1996 US 08/634325,13-JAN-1997 US 08/783520 PI  
KENNETH JACOBS, JOHN M MCCOY, LISA A RACIE, EDWARD R LAVALLIE, PI  
DAVID MERBERG.  
PC VIKRI SPAULDING  
FC C12N15/12,C07K14/47,A61K38/17  
CC Strandedness: Double;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
FEATURES  
source 1. .1778 Location/Qualifiers  
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/db\_xref="taxon:32630"

BASE COUNT 514 a 386 c 422 g 456 t

ORIGIN

Alignment Scores:  
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Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x BD105816 (1-1778)

Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
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707 ACAGCCTGATTATACGTTGAAGATGCAGAA 736

Db

RESULT 5  
AF119386  
LOCUS AF119386  
DEFINITION Homo sapiens blood plasma glutamate carboxypeptidase precursor (PGCP) mRNA, complete cds.  
ACCESSION AF119386  
VERSION AF119386.1 GI:4877697  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 1794)  
Gingras,R., Richard,C., El-Alfy,M., Morales,C.R., Potier,M. and Pehznetsky,A.V.  
Purification, cDNA cloning, and expression of a new human blood N-acetyl-aspartyl-alpha-glutamate plasma glutamate carboxypeptidase homologous to carboxypeptidase/prostate-specific membrane antigen  
J. Biol. Chem. 274 (17), 11742-11750 (1999)  
MEDLINE 99223495  
PUBMED 10206990  
2 (bases 1 to 1794)  
Gingras,R., Richard,C., El-Alfy,M., Morales,C.R., Potier,M. and Pehznetsky,A.V.  
Direct Submision  
Submitted (12-JAN-1999) Medical Genetics, Sainte-Justine Hospital, Montreal University, 3175 Cole Sainte-Catherine, Montreal, QU H3T 1C5, Canada

REFERENCE  
AUTHORS

TITLE

JOURNAL

FEATURES  
source 1. .1794 Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="8"  
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1. .1794  
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25. .1650  
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/RC\_number="3.4.17.21"  
/function="endopeptidase"  
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RASEARGKILVYNQPTGYEKTQVRYGAVAAKVGAVASLIQSVASFSIYSHTGIQ  
IOBYODGVPKIPACTIVEDAMEMSRMASRGNKIYIHLMEGAKTVPDTSFNTVAIT  
GSKYPRQVVLVSGHLDSDMDVGGAGNDGGAGFISWEALSLYKDLGRPLRLVLT  
AEBOGGVGAFOYIQLHKVNIINSYSLVMSDAGTFLPTGQFTGSEARAIMEVWLL  
QPLNTQVLSHSGTDINFWIAGVPPASLRDDIKYKFFFHSHGDMTMSIQSRML  
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sig\_peptide 25. .96



US-09-745-763-36\_COPY\_231\_240 (1-10) x BC037067 (1-1796)

Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
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 Db 747 ACAGCCTGTATACAGTGAAGATGCAGAA 776

# RESULT 7

BD106411 1851 bp DNA linear PAT 18-SEP-2002  
 LOCUS Secreted proteins and polynucleotides encoding them.

ACCESSION BD106411  
 VERSION BD106411.1 GI:23201229  
 KEYWORDS JP 2002503955-A/2.  
 SOURCE Chlamydia sp.  
 ORGANISM Chlamydia sp.

REFERENCE 1 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 1 (bases 1 to 1851)  
 AUTHORS Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,  
 Treacy,M., Spaulding,V. and Agostino,M.J.  
 TITLE Secreted proteins and polynucleotides encoding them  
 JOURNAL Patent: JP 2002503955-A 2 05-FEB-2002;  
 GENETICS INSTITUTE INC  
 COMMENT PN JP 2002503955-A/2  
 PD 05-FEB-2002  
 PF 20-MAR-1998 JP 1998545874  
 PR 21-MAR-1997 US 08/822167,19-MAR-1998 US 09/044466 PI  
 KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE,PI  
 DAVID MERBERG,  
 PI MAURICE TREACY,VIRKI SPAULDING,MICHAEL J AGOSTINO PC  
 C12N15/12,C07K14/47,A61K38/17  
 CC Strandedness: Double;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.

FEATURES  
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 /db\_xref="taxon:35827"

BASE COUNT 531 a 413 c 438 g 469 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 0.0125 Length: 1851  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x BD106411 (1-1851)

Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
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 Db 789 ACAGCCTGTATTACGCTGAAGATGCAGAA 818

RESULT 8  
 AX006440 1860 bp DNA linear PAT 06-SEP-2000  
 LOCUS Sequence 5 from Patent WO0004157.  
 ACCESSION AX006440  
 VERSION AX006440.1 GI:9994575  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Neefs,J.M., Peeters,D.C. and Pangalos,M.  
 TITLE Cloning and characterization of novel mammalian peptidases  
 JOURNAL Patent: WO 0004157-A 5 27-JAN-2000;  
 JANSSEN PHARMACEUTICA NV (BE); NEEFS JEAN MARC EDMOND FERNAND (BE);  
 PEETERS DANIELLE CELINE GEORGE (BE); PANGALOS MENIAS (GB)  
 FEATURES Location/Qualifiers

source 1..1860  
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 /db\_xref="taxon:9606"

BASE COUNT 518 a 420 c 451 g 471 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 0.0126 Length: 1860  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AX006440 (1-1860)

Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
 |||||  
 Db 815 ACAGCCTGTATTACGCTGAAGATGCAGAA 844

RESULT 9  
 BD127520 1860 bp DNA linear PAT 18-SEP-2002  
 LOCUS Primer for synthesizing full-length cDNA and use thereof.  
 DEFINITION BD127520  
 ACCESSION BD127520  
 VERSION BD127520.1 GI:23222465  
 KEYWORDS JP 2002017375-A/2951.  
 SOURCE JP 2002017375-A/2951.  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1860)  
 AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,  
 Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and  
 Koga,H.  
 TITLE Primer for synthesizing full-length cDNA and use thereof  
 JOURNAL Patent: JP 2002017375-A 2951 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002017375-A/2951  
 PD 22-JAN-2002  
 PF 07-JUL-2000 JP 2000253172.  
 PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO  
 PI ISHII,  
 PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,PI  
 SHINICHI KOJIMA,  
 PI TETSUJI OTSUKI,HISASHI KOGA  
 PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC

10', C12P21/02, C12P21/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
 Primer for synthesizing full-length cDNA and use thereof FH Key  
 Location/Qualifiers  
 FT CDS (129)..(1544).

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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x BD127520 (1-1860)

Oy 1 ThrAlaCyellThrValGluAspAlaGlu 10  
 DB 819 ACAGCCTGTATTACGCTGGAAGATCAGAA 848  
 RESULT 10  
 LOCUS AK075132  
 DEFINITION Homo sapiens cDNA FLJ90651.f1a, clone PLACE1004482, moderately similar to Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-tp) mRNA.  
 AK075132 1860 bp mRNA linear PRI 03-SEP-2002  
 ACCESSION AK075132.1 GI:22761022  
 VERSION AK075132.1  
 KEYWORDS oligo capping; f1s (full insert sequence).  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1  
 AUTHORS Isegai,T., Oca,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuno,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hatton,A., Okumura,K., Iwayanagi,T. and Nimomiya,K.  
 TITLE NEDO human cDNA sequencing project  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1860)  
 AUTHORS Isegai,T. and Otsuki,T.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-MAR-2002) Takao Isegai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
 COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.).  
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 ORIGIN  
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 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AK075132 (1-1860)  
 Oy 1 ThrAlaCyellThrValGluAspAlaGlu 10  
 DB 819 ACAGCCTGTATTACGCTGGAAGATCAGAA 848  
 RESULT 11  
 LOCUS BC020689  
 DEFINITION Homo sapiens, plasma glutamate carboxypeptidase, clone MGC:22418  
 IMAGE:4251802, mRNA, complete cds.  
 BC020689 1928 bp mRNA linear PRI 22-JAN-2002  
 ACCESSION BC020689.1 GI:18088383  
 VERSION BC020689.1  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1928)  
 AUTHORS Strausberg,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: http://mgc.nci.nih.gov  
 CONTACT: MGC help desk  
 Email: gga@nci.nih.gov  
 Tissue Procurement: ATCC/DCTD/DRP  
 CNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: http://www.sbgc.stanford.edu  
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov  
 Series: ILNL Plate: 35 Row: F Column: 13  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7706386.  
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 /note="Vector: pDNR-LIB"  
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 BASE COUNT 554 a 435 c 466 g 473 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 0.013 Length: 1928

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Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-745-763-36_COPY_231_240 (1-10) x BC020689 (1-1928)

Qy 1 ThrAlaCysGleThrValGluAspAlaGlu 10
Db 857 ACAGCCTGATTAAGTGGAAGATGAGAA 886

RESULT 12
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LOCUS Homo sapiens genomic DNA, chromosome 8q23, clone:KB1288E10.
ACCESSION AP003112
VERSION AP003112.1 GI:12362038
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 144703)
AUTHORS Shimizu, N. and Asakawa, S.
TITLE Homo sapiens chromosome clone KB1288E10 on 8q23
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 144703)
AUTHORS Shimizu, N. and Asakawa, S.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2001) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo
160-8582, Japan (E-mail: nshimizu@db.med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
Location/Qualifiers
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Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-745-763-36_COPY_231_240 (1-10) x AP003112 (1-144703)
Oy 1 ThrAlaCysIleThrValGluAspAlaGlu 10
Db 19498 ACAGCCTGTATTACGTGGAAGATGCAGAA 19527

RESULT 13
AP006278 157927 bp DNA linear PRI 25-MAR-2003
LOCUS Homo sapiens genomic DNA, chromosome 8q22.1, clone: KB1573B4,
DEFINITION complete sequence.
ACCESSION AP006278
VERSION AP006278.1 GI:29170583
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Shimizu,N. and Asakawa,S.
TITLE Homo sapiens DNA chromosome 8 SEQUENCE
JOURNAL Published Only in Database (2003)
REFERENCE 2 (bases 1 to 157927)
AUTHORS Shimizu,N. and Asakawa,S.
TITL Direct Submission
JOURNAL Submitted (24-MAR-2003) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
160-8582, Japan (E-mail:nshimizu@med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)

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29103. .29231 /evidence=not experimental
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35334. .35382 /evidence=not experimental
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Alignment Scores:
Pred. No.: 0.608 Length: 157927
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

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DB: 9 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AP006278 (1-157927)

Qy 1 ThralAcgttethrva1gluaSPAlaGlu 10

Db 144425 ACAGCCTGTATTACGCTGAGAGATGCAGAA 144454

RESULT 14

AC123654

LOCUS Mus musculus clone RP23-161D16, WORKING DRAFT SEQUENCE, 6 unordered pieces.

AC123654

AC123654.3 GI:28913182

VERSION HTG: HTGS PHASE1; HTGS\_DRAFT.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 203469)

Barren, B., Nusbaum, C. and Lander, E.

Mus musculus, clone RP23-161D16

Unpublished

2 (bases 1 to 203469)

Barren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatae, A., Kells, C., Larroque, K., Lamazares, R., Landers, T., Lenoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, D., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Niccol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Young, G., Zainoun, D., Zemdek, L., Zimmer, A. and Zody, M.

Young, G., Zainoun, D., Zemdek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 203469)

Barren, B., Nusbaum, C., Lander, E., Abouelell, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, B., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hales, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Niccol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rieback, M., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Stange, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, D., Zemdek, L., Zimmer, A. and Zody, M.

Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome

## COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 11, 2003 this sequence version replaced gt:28630056.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Project Information

Center Project name: L26344

Center Clone name: 161 D\_16

## ----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye, 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 201347 bases at least Q40

Consensus quality: 202412 bases at least Q30

Consensus quality: 202784 bases at least Q20

Insert size: 182000; agarose-fp

Insert size: 202969; sum-of-contigs

Quality coverage: 9.5 in Q20 bases; agarose-fp

Quality coverage: 8.5 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 34354: contig of 34354 bp in length

34355 34454: gap of 100 bp

34455 35050: contig of 596 bp in length

35051 35150: gap of 100 bp

35151 57072: contig of 21922 bp in length

57073 57172: gap of 100 bp

57173 72668: contig of 15496 bp in length

72669 72768: gap of 100 bp

72769 113967: contig of 41199 bp in length

113968 203469: gap of 100 bp

114068 203469: contig of 89402 bp in length.

## FEATURES

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1. 203463

/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

/clone="RP23-161D16"

/clone\_1b="RP23-161D16"

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/note="assembly\_fragment"

clone\_end:SP6

vector\_side:left"

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/note="assembly\_fragment"

35151..57072

/note="assembly\_fragment"

57173..72668

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72769..113967

/note="assembly\_fragment"

114068..203469

/note="assembly\_fragment"

clone\_end:T7

vector\_side:right"

BASE COUNT 63116 a 37616 c 37951 g 64286 t 500 others

ORIGIN

Alignment Scores: 0.759 Length: 203469

Pred. No.: 10.00 Matches: 10

Score:

Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%

Conservative: 0  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AC123654 (1-203469)

QY 1 ThrAlaCyseIleThrValaGluAspAlaGlu 10  
 Db 37215 ACAGCCTGTATTCACAGTAGAGATGCAGAA 37244

RESULT 15  
 AC129951/c

LOCUS Mus musculus clone RP23-127B14, WORKING DRAFT SEQUENCE, 5 unordered  
 DEFINITION pieces.

AC129951 214287 bp DNA linear HTG 06-MAR-2003  
 AC129951 GI:28667103  
 VERSION HTG: HTGS PHASE1; HTGS DRAFT.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 ORGANISM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 214287)  
 AUTHORS Birren,B., Nusbaum,C. and Lander,E.  
 TITLE Mus musculus, clone RP23-127B14  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 214287)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
 Barina,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,  
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,  
 Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
 Fero,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,  
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,  
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,  
 Karakas,A., Kellis,C., Landers,T., Levine,R., Lindblad-Toh,K.,  
 Liu,G., Maclean,C., Macdonald,P., Major,K., Matthews,C.,  
 McCarthy,M., Meldrum,J., Menus,L., Milhova,T., Menga,V.,  
 Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,  
 O'Connor,T., O'Donnell,F., O'Neill,D., Oliver,J., Peterson,K.,  
 Phunhthang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
 Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,  
 Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,D.,  
 Testfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,  
 Zembek,L., Zimer,A. and Zody,M.

Direct Submission  
 Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 REFERENCE 3 (bases 1 to 214287)

Birren,B., Nusbaum,C., Lander,E., Abouelkellil,A., Allen,N.,  
 Anderson,S., Arachchi,H.M., Barina,N., Bastien,V., Bloom,T.,  
 Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,  
 Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,  
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Fero,S.,  
 Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,  
 Graham,L., Grand-Pierre,N., Hagos,B., Haggopian,D., Hagos,B.,  
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
 Kamat,A., Karakas,A., Kellis,C., Landers,T., Levine,R.,  
 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,  
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
 Meldrum,J., Menus,L., Milhova,T., Menga,V., Murphy,T., Naylor,J.,  
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,F.,  
 O'Neill,D., Oliver,J., Peterson,K., Phunhthang,P., Pierre,N.,  
 Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
 Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,  
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
 Talamas,J., Testfaye,S., Theodore,J., Topham,K., Travers,M.,  
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimer,A. and Zody,M.

TITLE  
 JOURNAL

Submitted (06-MAR-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

## COMMENT

On Mar 6, 2003 this sequence version replaced gi:28604146.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/XM/RepeatMasker.html>

## Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

## Project Information

Center project name: L26330  
 Center clone name: 127\_B\_14

## Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 213323 bases at least Q40  
 Consensus quality: 213594 bases at least Q30  
 Consensus quality: 213779 bases at least Q20  
 Insert size: 21000; agarose-fp  
 Insert size: 213887; sum-of-ctigs  
 Quality coverage: 8.3 in Q20 bases; agarose-fp  
 Quality coverage: 8.2 in Q20 bases; sum-of-ctigs

NOTE: This is a 'working draft' sequence. It currently  
 consists of 5 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 96711: contig of 96711 bp in length  
 \* 96712 96811: gap of 100 bp  
 \* 96812 113998: contig of 1787 bp in length  
 \* 113999 114098: gap of 100 bp  
 \* 114099 138884: contig of 24786 bp in length  
 \* 138885 138984: gap of 100 bp  
 \* 138985 210099: contig of 7115 bp in length  
 \* 210100 210199: gap of 100 bp  
 \* 210200 214287: contig of 4088 bp in length.

## FEATURES

## source

1. 214287  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /clone="RP23-127B14"  
 /clone\_1lb="RPCT-23 Female Mouse BAC"  
 1. 96711  
 /note="assembly\_fragment"  
 misc\_feature 96812..113998  
 /note="assembly\_fragment"  
 misc\_feature 114099..138884  
 /note="assembly\_fragment"  
 misc\_feature 138985..210099  
 /note="assembly\_fragment"  
 misc\_feature 210200..214287  
 /note="assembly\_fragment"  
 clone\_end: 27  
 vector\_side:right"

BASE COUNT 67592 a 41331 c 41087 g 63872 t 405 others  
 ORIGIN

## Alignment Scores:

Score: 0.794 Length: 214287  
 Pred. No.: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AC129951 (1-214287)

Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
| | | | | | | | | | | | | | | | | |  
Db 94648 ACAGCCTGTATCATCAGCTGTAAGAAATGCAGAA 94619

Search completed: December 23, 2003, 13:06:21  
Job time : 1517 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM-protein - nucleic search, using frame\_plus\_p2n model

Run on: December 23, 2003, 12:00:30 ; Search time 256 Seconds  
(without alignments)  
105.447 Million cell updates/sec

Title: US-09-745-763-36\_COPY\_231\_240  
Sequence: 1 TACTIVEDAR 10

Scoring table:  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5087518

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xip  
-Q=/cgn2.1/USPTO.spool\_p/US09745763/runat\_23122003.120023.20072/app\_query.fasta.1.199  
-DB=N Geneseq.19jun03 -OPMT=fastap -SUFFIX=olip2n.rng -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=coligo -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09745763.@CGN.1.1.490@runat\_23122003.120023.20072 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

N\_Geneseq.19jun03: \*  
1: /SIDSI/gcgdata/geneseq/geneseg-emb1/NA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseg-emb1/NA1981.DAT.\*  
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18: /SIDSI/gcgdata/geneseq/geneseg-emb1/NA1997.DAT.\*  
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24: /SIDSI/gcgdata/geneseq/geneseg-emb1/NA2003.DAT.\*  
25: /SIDSI/gcgdata/geneseq/geneseg-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	895	21	Human secreted exp
2	10	100.0	1134	21	Human secreted pro
3	10	100.0	1134	22	Human secreted pro
4	10	100.0	1134	24	Human secreted pro
5	10	100.0	1134	25	Human secreted pro
6	10	100.0	1134	25	Human secreted pro
7	10	100.0	1767	21	Human secreted pro
8	10	100.0	1767	18	Human secreted pro
9	10	100.0	1767	18	Human secreted pro
10	10	100.0	1767	23	Human secreted pro
11	10	100.0	1851	19	Human secreted pro
12	10	100.0	1851	24	Human secreted pro
13	10	100.0	1851	24	Human secreted pro
14	10	100.0	1851	24	Human secreted pro
15	10	100.0	1851	24	Human secreted pro
16	10	100.0	1851	24	Human secreted pro
17	10	100.0	1851	24	Human secreted pro
18	10	100.0	1851	24	Human secreted pro
19	10	100.0	1851	24	Human secreted pro
20	10	100.0	1851	24	Human secreted pro
21	10	100.0	1851	24	Human secreted pro
22	10	100.0	1851	24	Human secreted pro
23	10	100.0	1851	24	Human secreted pro
24	10	100.0	1851	24	Human secreted pro
25	10	100.0	1851	24	Human secreted pro
26	10	100.0	1851	24	Human secreted pro
27	10	100.0	1851	24	Human secreted pro
28	10	100.0	1851	24	Human secreted pro
29	10	100.0	1851	24	Human secreted pro
30	10	100.0	1851	24	Human secreted pro
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32	10	100.0	1851	24	Human secreted pro
33	10	100.0	1851	24	Human secreted pro
34	10	100.0	1851	24	Human secreted pro
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37	10	100.0	1851	24	Human secreted pro
38	10	100.0	1851	24	Human secreted pro
39	10	100.0	1851	24	Human secreted pro
40	10	100.0	1851	24	Human secreted pro
41	10	100.0	1851	24	Human secreted pro
42	10	100.0	1851	24	Human secreted pro
43	10	100.0	1851	24	Human secreted pro
44	10	100.0	1851	24	Human secreted pro
45	10	100.0	1851	24	Human secreted pro

## ALIGNMENTS

RESULT 1  
AAAA4369 standard; CDNA; 895 BP.  
AC AAA44369;  
XX  
XX 21-AUG-2000 (first entry)  
XX  
XX Human secreted expressed sequence tag SEQ ID NO:944.  
XX Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;  
XX expressed sequence tag; SEST; probe; chemotactic; proliferative;  
XX immunomodulatory; haematopoietic; chemokine; anastatic; haematoc;  
XX thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;  
XX antiviral; antidiabetic; antiaslomatic; vulnerary; antiparisonant;  
XX antitumor; osteoprotective; neuroprotective; nootropic; antipsychotic;  
XX cerebroprotective; anticonvulsant; antidepressant; gene therapy;

KM vaccine; autoimmune disorder; multiple sclerosis; allergic condition;  
 KM insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;  
 KM lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;  
 KM central nervous system disorder; Alzheimer's disease; stroke;  
 KM Parkinson's disease; Huntington's disease; coagulation disorder;  
 KM hemophilia; thrombosis; inflammatory disorder; Crohn's disease;  
 KM tumour; infection; depression; psoriasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200021991-A1.  
 PD 20-APR-2000.  
 XX  
 PF 15-OCT-1999; 99WO-US24206.  
 XX  
 PR 15-OCT-1998; 98US-0104436.  
 XX  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;  
 PI Metberg D, Treacy M, Bowman MR;  
 XX  
 DR WPI: 2000-317938/27.  
 XX  
 PT Isolated polynucleotides, and encoded proteins, comprising secreted  
 PT expressed sequence tags (ESTs), useful for treating various disorders  
 PT such as autoimmune, infectious, and central nervous system disorders -  
 XX  
 PS Claim 1; Page 446; 803bp; English.  
 XX  
 AA443426 to AA45925 represent specifically claimed secreted expressed  
 CC sequence tags (ESTs), isolated from human, mouse, chicken and rat  
 CC tissue sources. The ESTs can have a range of activities depending on  
 CC the tissues they were isolated from. The activities include:  
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;  
 CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;  
 CC cyostatic; antibacterial; antifungal; antiviral; antidiabetic;  
 CC antiaesthetic; vulnerary; antitumor; osteoprotective; neuroprotective;  
 CC nociceptive; antiparkinsonian; antipsoriatic; cerebroprotective;  
 CC anticonvulsant; and antidepressant. The ESTs can be used for gene  
 CC therapy and in vaccines. The ESTs are useful as probes for the  
 CC identification and isolation of full-length cDNAs and genomic DNA  
 CC molecules which correspond to the ESTs. Proteins encoded by the ESTs  
 CC are useful in assays for determining biological activity and raising  
 CC antibodies. They may be useful for treatment of autoimmune disorders  
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions  
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,  
 CC osteoporosis, osteoarthritis, central nervous system disorders  
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation  
 CC disorders (hemophilia, thrombosis), inflammatory disorders (Crohn's  
 CC disease), tumours, bacterial, fungal or viral infections, depression and  
 CC psoriasis. AA443426 to AA45925 represent linker variants which are given  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 895 BP; 274 A; 195 C; 224 G; 201 T; 1 other;

Alignment Scores:  
 Pred. No.: 0.01 Length: 895  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 10  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AA444369 (1-895)  
 Oy 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
 Db 734 ACAGCCTGATTTACGCTGAGAGATGACGAA 763  
 RESULT 2  
 AA298101

ID AA298101 standard; cDNA; 1134 BP.  
 XX  
 AC AA298101;  
 XX  
 DT 09-MAY-2000 (first entry)  
 XX  
 DE Human secreted protein encoding nucleotide sequence SEQ ID NO:95.  
 XX  
 KW Human; secreted protein; diagnosis; cyostatic; immunosuppressive;  
 KW antiinflammatory; nociceptive; neuroprotective; antiallergic; cancer;  
 KW tumour; neurodegenerative disorder; developmental abnormality; allergy;  
 KW foetal deficiency; blood disorder; immune system disorder; arthritis;  
 KW autoimmune disease; hepatic disease; renal disease; inflammation;  
 KW Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis;  
 KW infection; AIDS; spinal cord injury; transplant rejection; diabetes;  
 KW asthma; sepsis; acne; psoriasis; cardiovascular disorder;  
 KW reproductive disorder; gastrointestinal disorder; respiratory disorder;  
 KW metabolic disorder; food additive; preservative; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200004140-A1.  
 PD 27-JAN-2000.  
 XX  
 PF 14-JUL-1999; 99WO-US15849.  
 XX  
 PR 15-JUL-1998; 98US-0092921.  
 PR 15-JUL-1998; 98US-0092922.  
 PR 15-JUL-1998; 98US-0092956.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Komatsoulis G, Duan RD, Rosen CA, Moore PA, Shi Y;  
 PI Lafleur DW, Edder R, Olsen HS, Brewer LA, Florence KA, Young PB;  
 PI Mucenski M, Endress GA, Soppet DR;  
 DR WPI: 2000-161128/14.  
 DR P-PSDB; AA67148.  
 XX  
 PT New isolated human genes, useful for diagnosis and treatment of, e.g.  
 PT cancers, neurological or blood disorders -  
 XX  
 PS Claim 1; Page 365; 494bp; English.  
 XX  
 The polynucleotide sequences given in AA298017 to AA298108 encode the  
 CC human secreted proteins given in AA187064 to AA187223. Human secreted  
 CC protein can have activities based on the tissues and cells the genes are  
 CC expressed in. Examples of activities include: cyostatic;  
 CC immunosuppressive; antiinflammatory; nociceptive; neuroprotective; and  
 CC antiallergic. The polynucleotides and their corresponding secreted  
 CC polypeptides are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g. by protein or gene therapy. Also pathological conditions  
 CC can be diagnosed by determining the amount of the new polypeptides in a  
 CC sample or by determining the presence of mutations in the new  
 CC polynucleotides. Human secreted proteins and their polynucleotides can  
 CC be used for developing products for the diagnosis or treatment of cancer,  
 CC tumours, neurodegenerative disorders, developmental abnormalities and  
 CC foetal deficiencies, blood disorders, diseases of the immune system,  
 CC autoimmune diseases, hepatic and renal disease, inflammation,  
 CC allergies, Alzheimer's disease, behavioural disorders, schizophrenia,  
 CC osteoporosis, arthritis, infections, AIDS, spinal cord injuries,  
 CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,  
 CC cardiovascular disorders, reproductive disorders, gastrointestinal  
 CC disorders, respiratory disorders and metabolic disorders. The  
 CC proteins or polynucleotides can also be used as food additives or  
 CC preservatives. The proteins are also useful for identifying their  
 CC binding partners. AA298008 to AA298016 and AA187063 are sequence used in  
 CC the exemplification of the present invention.  
 XX  
 SQ Sequence 1134 BP; 333 A; 247 C; 250 G; 304 T; 0 other;

Alignment Scores:

Pred. No.: 0.0123 Length: 1134  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AA298101 (1-1134)  
 QY 1 ThrAlaCyeIleThrValGluAspAlaGlu 10  
 Db 61 ACAGCCTGTATTACGGTGAAGATGCGAAG 90

RESULT 3  
 AAD11714  
 ID AAD11714 standard; cDNA; 1134 BP.  
 AC AAD11714;  
 XX 24-SEP-2001 (first entry)  
 DT  
 XX Human secreted protein-encoding gene 18 cDNA clone HMAA234, SEQ ID NO:95.  
 XX  
 KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;  
 KW poriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;  
 KW inflammation; neurological disorder; Alzheimer's disease; food additive;  
 KW angiotensin disorder; kidney disorder; gastrointestinal disorder; allergy;  
 KW pregnancy-related disorder; endocrine disorder; infection; wound healing;  
 KW cell culture; chemotaxis; vulnery; binding partner identification;  
 KW gene therapy; ss.  
 KM  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 687..788  
 FT /\*tag= a  
 FT /product= "Human secreted protein precursor"  
 FT  
 XX WO200151504-A1.  
 PN 19-JUL-2001.  
 XX  
 PF 12-JAN-2001; 2001WO-US00911.  
 XX  
 PR 13-JAN-2000; 2000US-0482273.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Komatsoulis GA, Duan DR, Rosen CA, Moore PA, Shi Y,  
 PI Lafleur DM, Olsen HS, Brewer LA, Florence KA, Young PE, Soppet DR;  
 PI Endress GA, Muscenski M, Ebner R;  
 XX  
 XX WPI: 2001-425865/45.  
 DR P-PSDB; AAE06125.  
 DR  
 XX Isolated nucleic acid molecule encoding a human secreted protein is  
 PT used in preventing, treating or ameliorating a medical condition -  
 XX  
 PS Claim 1; Page 732; 864pp; English.  
 XX  
 CC AAD1630-AAD11721 represent cDNAs corresponding to 71 human secreted  
 CC protein genes, and AAE06041-AAE06132 represent the proteins they encode.  
 CC AAE06133-AAE06205 represent human secreted protein fragments.  
 CC The secreted proteins and their genes are useful for preventing, treating  
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.  
 CC Pathological conditions can be diagnosed by determining the amount of the  
 CC new protein in a sample or by determining the presence of mutations in  
 CC the new genes. Specific uses are described for each of the 71 genes,  
 CC based on the tissues in which they are most highly expressed, and include  
 CC developing products for the diagnosis or treatment of proliferative

CC disorders, cancer, tumours, foetal and developmental abnormalities,  
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune  
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, autoimmune  
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),  
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,  
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,  
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,  
 CC pregnancy-related disorders, endocrine disorders, and infections. The  
 CC proteins can also be used to aid wound healing and epithelial cell  
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
 CC before transplantation, for supporting cell culture of primary tissues,  
 CC to regenerate tissues, to identify their cognate ligands or binding  
 CC partners, and in chemotaxis, and can be used as a food additive or  
 CC preservative to modify storage properties. Antibodies specific for a  
 CC protein of the invention can be used in alleviating symptoms associated  
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,  
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).  
 CC The present sequence represents a human secreted protein-encoding cDNA of  
 CC the invention.  
 XX  
 SO Sequence 1134 BP; 333 A; 247 C; 250 G; 304 T; 0 other;

Alignment Scores:  
 Pred. No.: 0.0123 Length: 1134  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AAD11714 (1-1134)  
 QY 1 ThrAlaCyeIleThrValGluAspAlaGlu 10  
 Db 61 ACAGCCTGTATTACGGTGAAGATGCGAAG 90

RESULT 4  
 ABR69810  
 ID ABR69810 standard; cDNA; 1134 BP.  
 AC ABR69810;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human secreted protein gene 18 #2.  
 XX  
 XX Human; ss; gene; secreted protein; gene therapy; immunosuppressive;  
 KW antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac;  
 KW vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;  
 KW virucide; fungicide; ophthalmological; autoimmune disease; neoplasm;  
 KW rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;  
 KW cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;  
 KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;  
 KW ocular disorder; corneal infection; wound healing; skin aging;  
 KW epithelial cell proliferation; food additive.  
 KM  
 OS Homo sapiens.  
 XX  
 PN WO200226931-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 24-SEP-2001; 2001WO-US29871.  
 XX  
 PR 25-SEP-2000; 2000US-234925P.  
 XX  
 PR 12-JAN-2001; 2001WO-US00911.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Komatsoulis G, Duan DR, Rosen CA, Moore PA, Shi Y,  
 PI Lafleur DM, Olsen H, Brewer LA, Florence KA, Young PE, Soppet DR,  
 PI Endress GA, Muscenski M, Ebner R;  
 XX

DR WPI; 2002-362489/39.  
DR P-PSDB; ABG33947.  
XX  
PT Novel 71 isolated secreted polypeptides and polynucleotides encoding  
PT the polypeptides, useful for treating Huntington's disease, sepsis,  
PT meningitis, thrombocytopenia, haemolytic anaemia, rheumatoid arthritis,  
PT asthma  
XX  
PS Claim 1; Page 1213-1214, 1478pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (or its  
CC fragment, homologue complement or allelic variant) encoding a human  
CC secreted protein (and its fragment, domain, epitope, variant, secreted  
CC form and species variant). Also included are a recombinant vector  
CC comprising the nucleic acid, a recombinant host cell comprising the  
CC vector, an antibody against the secreted protein, a recombinant host cell  
CC that expresses the secreted protein and a method of identifying a binding  
CC partner of the secreted protein. The nucleic acid and protein are used to  
CC prevent, diagnose, treat or ameliorate a medical condition in e.g.  
CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep  
CC for example autoimmune diseases e.g. rheumatoid arthritis,  
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
CC e.g. cerebral ischaemia, angiodenesis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and  
CC ocular disorders e.g. corneal infection. Many other diseases and  
CC disorders are listed in the specification. The polypeptides can also be  
CC used to aid wound healing an epithelial cell proliferation, to prevent  
CC skin aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis. The polypeptides can also be used as a food additive or  
CC preservative to increase or decrease storage capabilities. The present  
CC sequence encodes a novel human secreted protein of the invention.  
XX  
SQ Sequence 1134 BP, 333 A; 247 C; 250 G; 304 T; 0 other;  
SQ  
Alignment Scores:  
Pred. No.: 0.0123 Length: 1134  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
US-09-745-763-36\_COPY\_231\_240 (1-10) x ABK69810 (1-1134)  
CY 1 ThrAaCysIleThrValGluAspAlaGlu 10  
Db 61 ACAGCCTGTATTACGGTGGAGATGCAGAA 90  
RESULT 5  
ACCS0818  
ID ACCS0818 standard; cDNA; 1134 BP.  
XX  
AC ACCS0818;  
XX  
DT 12-JUN-2003 (first entry)  
DE Human secreted protein coding sequence, SEQ ID 485.  
XX  
KM Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cyostatic;  
KM vulnery; antiinflammatory; nootropic; neuroprotective;  
KM antiparkinsonian; gene therapy; human; cardiovascular disorder;  
KM gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200295010-A2.  
XX  
PD 28-NOV-2002.  
XX  
PF 19-MAR-2002; 2002WO-US09785.  
XX

PR 21-MAR-2001; 2001US-277340P.  
PR 19-JUL-2001; 2001US-306171P.  
PR 13-NOV-2001; 2001US-331287P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2003-129429/12.  
XX  
XX  
PT Novel human secreted proteins, useful for detecting, preventing,  
PT diagnosing, prognosticating, treating and/or ameliorating  
PT cardiovascular disorders such as arrhythmia  
XX  
PS Claim 21; SEQ ID 485; 1881pp; English.  
XX  
CC The present invention relates to novel human secreted proteins  
CC (ABR47633-ABR48145) and their coding sequences (ACCS0344-ACCS0856). The  
CC proteins and their coding sequences are useful for the preparation of a  
CC diagnostic or pharmaceutical composition for diagnosing or treating a  
CC cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest,  
CC coronary arteriosclerosis and myocardial ischaemia), neural disorders,  
CC immune system disorders, muscular disorders, reproductive disorders,  
CC gastrointestinal disorders, pulmonary disorders, renal disorders,  
CC proliferative disorders and/or cancerous diseases and conditions, for  
CC wound healing and epithelial cell proliferation, to treat inflammation or  
CC infection, for treating thrombosis and arteriosclerosis, for treating or  
CC preventing neural damage which occurs in neuronal disorders or  
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's  
CC disease, to enhance bone and periodontal regeneration and aid in tissue  
CC transplants or bone grafts, to prevent skin aging or hair loss, to  
CC stimulate growth and differentiation of haematopoietic cells and bone  
CC marrow cells when used in combination with other cytokines, to maintain  
CC organs before transplantation or for supporting cell culture of primary  
CC tissues, to increase or decrease differentiation or proliferation of  
CC embryonic stem cells, or to modulate mammalian characteristics or  
CC metabolism.  
CC Note: The sequence data for this patent was published in electronic  
CC format and is available from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 1134 BP, 333 A; 247 C; 250 G; 304 T; 0 other;  
SQ  
Alignment Scores:  
Pred. No.: 0.0123 Length: 1134  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 25 Gaps: 0  
US-09-745-763-36\_COPY\_231\_240 (1-10) x ACCS0818 (1-1134)  
CY 1 ThrAaCysIleThrValGluAspAlaGlu 10  
Db 61 ACAGCCTGTATTACGGTGGAGATGCAGAA 90  
RESULT 6  
ABZ71454  
ID ABZ71454 standard; cDNA; 1134 BP.  
XX  
AC ABZ71454;  
XX  
DT 04-APR-2003 (first entry)  
DE Secreted protein-encoding gene 142 cDNA clone HRAUCJ35, SEQ ID NO:275.  
XX  
XX  
KM Human; secreted protein; digestive disorder; gastrointestinal disorder;  
KM mouth; oesophagus; stomach; small intestine; large intestine; liver;  
KM biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;  
KM immune disorder; inflammation; infection; wound healing; drug screening;  
KM chromosome identification; chromosome mapping; cyostatic;  
KM antiinflammatory; immunosuppressive; vulnery; gene therapy; gene; ss.



XX Homo sapiens.  
 OS  
 XX  
 PN MO200276488-A1.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 19-MAR-2002; 2002WO-US08276.  
 XX  
 PR 21-MAR-2001; 2001US-277340P.  
 PR 19-JUL-2001; 2001US-306171P.  
 PR 13-NOV-2001; 2001US-331287P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2003-029900/02.  
 DR P-PSDB; ABR00275.  
 XX  
 PT New human secreted proteins and nucleic acids, useful for detecting,  
 PT preventing, diagnosing, prognosticating, treating and/or ameliorating  
 PT e.g. gastrointestinal diseases and disorders, or cancers -  
 XX  
 PS Claim 21; Page 918-919; 1216pp; English.  
 XX  
 CC ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted  
 CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.  
 CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The  
 CC invention also encompasses antibodies specific for the secreted proteins,  
 CC the use of the secreted proteins in drug screening, and recombinant  
 CC vectors and host cells comprising a nucleic acid of the invention. The  
 CC secreted proteins, nucleic acids encoding them, antibodies or antibody  
 CC fragments are useful for the secreted proteins, and modulators of protein  
 CC activity are useful for diagnosing, treating, ameliorating or preventing  
 CC digestive disorders. Such conditions include disorders of the mouth,  
 CC oesophagus, stomach, small intestine, large intestine, liver, biliary  
 CC tract and pancreas, and include cancers of these organs and tissues. The  
 CC secreted proteins and their nucleic acids may also be used in the  
 CC treatment of immune disorders, inflammation, infection,  
 CC hyperproliferative disorders, and to promote wound healing. Nucleic acids  
 CC of the invention may be used for chromosome identification, chromosome  
 CC mapping, in gene therapy, for identifying individuals from minute  
 CC biological samples, as hybridisation probes, and as molecular weight  
 CC markers. The present sequence represents a human secreted protein-  
 CC encoding cDNA clone of the invention.  
 CC  
 XX SQ Sequence 1134 BP; 333 A; 247 C; 250 G; 304 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 0.0123 Length: 1134  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 25 Gaps: 0  
 US-09-745-763-36\_COPY\_231\_240 (1-10) x ABZ71454 (1-1134)  
 QY 1 ThTAlaCysElleThrValGluAspAlaGlu 10  
 Db 61 ACAGCCTGTTTACGCTGGAAGATGCAGAA 90  
 RESULT 7  
 ID AAA40493 standard; cDNA; 1767 BP.  
 XX  
 AC AAA40493;  
 XX  
 XX 16-NOV-2000 (first entry)  
 XX  
 DE Human fetal kidney cDNA fragment AM282\_11.  
 XX

KM Secreted protein; cytostatic; immunostimulatory; antimicrobial;  
 KM antiviral; immunosuppressive; antiinflammatory; vulnerary; cytokine;  
 KM cell proliferation; differentiation; regulatory; treatment; tumor;  
 KM autoimmune disease; inflammatory disorder; wound; microbial infection;  
 KM viral disease; graft versus host reaction suppression; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200037630-A1.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PF 22-DEC-1999; 99WO-US31005.  
 XX  
 PR 23-DEC-1998; 98US-0220876.  
 XX  
 PA (GEMY) GENETICS INST INC.  
 XX  
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C,  
 PI Merberg D, Treacy M, Bowman MR;  
 XX  
 DR WPI; 2000-442661/38.  
 DR P-PSDB; AAB10229.  
 XX  
 PT Secreted human proteins AS296-11 and AS34-11, useful for treating  
 PT tumors, autoimmune diseases, inflammatory disorders, wounds, microbial  
 PT infections and viral diseases -  
 XX  
 PS Disclosure; Page 198; 293pp; English.  
 XX  
 CC This invention describes novel secreted human proteins (I) which have  
 CC cytostatic, immunostimulatory, antimicrobial, antiviral,  
 CC immunosuppressive, antiinflammatory and vulnerary activity and which act  
 CC as cytokine, cell proliferation or differentiation regulators. (I)  
 CC is useful for treating tumors, autoimmune diseases, inflammatory  
 CC disorders, wounds, microbial infections and viral diseases. (I) is also  
 CC useful for suppressing graft versus host reaction. AAA40490-AA0580  
 CC represent cDNA fragments that encode the secreted proteins  
 CC AAB10226-B10288 described in the method of the invention.  
 CC  
 XX SQ Sequence 1767 BP; 512 A; 384 C; 418 G; 453 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 0.0179 Length: 1767  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0  
 US-09-745-763-36\_COPY\_231\_240 (1-10) x AAA40493 (1-1767)  
 QY 1 ThTAlaCysElleThrValGluAspAlaGlu 10  
 Db 696 ACAGCCTGTTTACGCTGGAAGATGCAGAA 725  
 RESULT 8  
 ID AAV02296 standard; DNA; 1778 BP.  
 XX  
 AC AAV02296;  
 XX  
 XX 21-MAY-1998 (first entry)  
 XX  
 DE Human secreted protein AM282 full-length cDNA clone.  
 XX  
 KM Secreted protein; AM282; cytokine; human; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FH 17..1435  
 FT CDS /\*tag= a  
 FT

FT sig\_peptide 17..88  
 FT /\*tag= b  
 FT mat\_peptide 89..1432  
 FT /\*tag= b  
 XX  
 XX WO9739030-A2.  
 XX  
 XX 23-OCT-1997.  
 XX  
 XX 16-APR-1997; 97WO-US06475.  
 XX  
 XX 13-JAN-1997; 97US-0783520.  
 XX 18-APR-1996; 96US-0634325.  
 XX  
 XX (GEMV ) GENETICS INST INC.  
 XX  
 XX Jacobs K, LaVallie ER, McCoy JM, Merberg D, Racie LA,  
 XX Spaulding V;  
 XX WPI: 1997-526400/48.  
 XX P-PSDB; AAM33604.  
 XX  
 XX New isolated secretory proteins AM340, AM282 and AK583 - possibly  
 PT have cytokine, cell proliferation/differentiation regulating,  
 PT immunomodulating activities, etc.  
 XX  
 XX Claim 15: Page 44-45; 59pp; English.  
 XX  
 XX This cDNA clone encodes a protein (see W33604) designated AM282.  
 CC It was identified as "y195b10.r1 human EST 30142 5" (Genbank  
 CC accession No. R77830) in a database search using a partial AM282  
 CC clone (see T97398) obtained from a human foetal kidney cDNA  
 CC library using methods selective for cDNAs encoding secreted  
 CC proteins. AM282 is deposited in ATCC 98026 together with clones  
 CC AM340 (see T97387) and AK583 (see V02297), which are also claimed.  
 CC AM282 protein can be used in a claimed method for preventing,  
 CC treating or ameliorating a medical condition. It may exhibit  
 CC cytokine, cell proliferation (either inducing or inhibiting) or  
 CC cell differentiation (either inducing or inhibiting) activity or  
 CC may induce production of other cytokines in certain cell  
 CC populations. It may also exhibit e.g. immune stimulating or  
 CC suppressing activity, haematopoiesis regulating activity, tissue  
 CC growth activity, activin/inhibin activity, chemotactic or  
 CC chemokinetic activity, haemostatic or thrombolytic activity,  
 CC receptor/ligand activity, anti-inflammatory activity, tumour  
 CC inhibition activity, or other activities. No evidence of any of  
 CC these activities is given in the specification.  
 XX  
 XX Sequence 1778 BP; 514 A; 386 C; 422 G; 456 T; 0 other;  
 XX  
 XX Alignment Scores:  
 SQ Pred. No.: 0.018 Length: 1778  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 18 Gaps: 0  
 US-09-745-763-36\_COPY\_231\_240 (1-10) x AAV02296 (1-1778)  
 QY 1 ThralaCysilethrrValGluAspAlaGlu 10  
 Db 707 ACAGCCTGTATTACGTCGGAAGATCGACGA 736  
 RESULT 9  
 ID AAS73592 standard; cDNA; 1784 BP.  
 XX  
 XX AAS73592;  
 AC  
 XX 13-FEB-2002 (first entry)  
 XX  
 XX DNA encoding novel human diagnostic protein #9396.  
 DE

XX  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200175067-A2.  
 XX  
 XX 11-OCT-2001.  
 XX  
 XX 30-MAR-2001; 2001WO-US08631.  
 XX  
 XX 31-MAR-2000; 2000US-0540217.  
 XX 23-AUG-2000; 2000US-0649167.  
 XX  
 XX (HYSE-) HYSEO INC.  
 XX  
 XX Drmanac RT, Liu C, Tang YT;  
 XX WPI: 2001-639362/73.  
 XX P-PSDB; ABG09405.  
 XX  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 XX  
 XX Claim 1; SEQ ID No 9396; 103pp; English.  
 XX  
 XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human  
 CC diagnostic coding sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 1784 BP; 508 A; 389 C; 426 G; 461 T; 0 other;  
 XX  
 XX Alignment Scores:  
 SQ Pred. No.: 0.018 Length: 1784  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 23 Gaps: 0  
 US-09-745-763-36\_COPY\_231\_240 (1-10) x AAS73592 (1-1784)  
 QY 1 ThralaCysilethrrValGluAspAlaGlu 10  
 Db 691 ACAGCCTGTATTACGTCGGAAGATCGACGA 720  
 RESULT 10  
 ID AAV82779 standard; cDNA; 1851 BP.  
 XX  
 XX AAV82779;  
 AC  
 XX  
 XX AAV82779;  
 XX

DT 25-FEB-1999 (first entry)  
 XX  
 DE Clone hu45\_2 isolated from human adult placenta cDNA library.  
 XX  
 KW Secreted protein; nutritional activity; immune stimulating; vaccine;  
 KW suppressing activity; haematopoiesis regulating activity;  
 KW tissue growth activity; activin; inhibin activity; chemotaxis;  
 KW chemokinetic activity; haemostasis; thrombolytic activity; receptor;  
 KW ligand; anti-inflammatory; cadherin; tumour invasion suppressor;  
 KW tumour inhibition; gene therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN M09842739-A2.  
 XX  
 PD 01-OCT-1998.  
 XX  
 PF 20-MAR-1998; 98WO-US05653.  
 XX  
 PR 19-MAR-1998; 98US-0044466.  
 PR 21-MAR-1997; 97US-0822167.  
 XX  
 PA (GENY) GENETICS INST INC.  
 XX  
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;  
 PI Racie LA, Spaulding V, Treacy M;  
 XX  
 DR WPI; 1998-609890/51.  
 DR P-PSDB; AAW85456.  
 XX  
 PT New polynucleotide encoding secreted human proteins - derived from  
 PT human foetal brain, adult brain, foetal kidney, placenta or adult  
 PT pineal gland cDNA libraries.  
 XX  
 PS Claim 14; Page 69-70; 113pp; English.  
 XX  
 CC The present sequence encodes a secreted protein. The polynucleotide and  
 CC secreted protein are predicted to have biological activities which would  
 CC make them suitable for treating, preventing or ameliorating medical  
 CC conditions in humans and animals, although no supporting data is given.  
 CC Suggested activities include nutritional activity, immune stimulating  
 CC (e.g. as vaccines) or suppressing activity, haematopoiesis regulating  
 CC activity, tissue growth activity, activin/inhibin activity,  
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,  
 CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour  
 CC invasion suppressor activity, and tumour inhibition activity (no data is  
 CC given in the specification to support these activities). The  
 CC polynucleotide is also stated to be useful for gene therapy.  
 XX  
 SQ Sequence 1851 BP; 531 A; 413 C; 438 G; 469 T; 0 other;  
 XX  
 Alignment Scores:  
 Pred. No.: 0.0186 Length: 1851  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0  
 XX  
 US-09-745-763-36\_COPY\_231\_240 (1-10) x AAV82779 (1-1851)  
 QY 1 ThrAlaCysIleTrrValGluAspAlaGlu 10  
 Db 789 ACAGCCTGTATTACGTGGAAGATGCAGAA 818  
 XX  
 RESULT 11  
 ABQ92016 ID ABQ92016 standard; cDNA; 1851 BP.  
 AC ABQ92016;  
 XX  
 DT 04-OCT-2002 (first entry)  
 XX

DE Human polynucleotide SEQ ID NO 13.  
 XX  
 KW Human; cytostatic; antirheumatic; antiarthritic; vulnereary; analgesic;  
 KW antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;  
 KW neuroprotective; nootropic; osteopathic; haemostatic; vasotropic;  
 KW antidiacer; fungicide; antidiabetic; antiallergic;  
 KW immunostimulant; antiparasitic; secreted protein; transmembrane protein;  
 KW cytokine; cell proliferation; cell differentiation; autoimmune disease;  
 KW stem cell; growth factor; nervous system disease; neuropathy;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW osteoporosis; severe combined immunodeficiency; SCID; infection;  
 KW multiple sclerosis; rheumatoid arthritis; gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002065394-A1.  
 XX  
 PD 30-MAY-2002.  
 XX  
 PF 22-DEC-2000; 2000US-0745763.  
 XX  
 PR 18-MAR-1998; 98US-0040963.  
 XX  
 PA (JACO/) JACOBS K.  
 PA (MCCO/) MCCOY J M.  
 PA (LAVA/) LAVALLIE E R.  
 PA (COLL/) COLLINS-RACIE L A.  
 PA (EVAN/) EVANS C.  
 PA (MERB/) MERBERG D.  
 PA (TREAC/) TREACY M.  
 PA (SPAUV/) SPAULDING V.  
 XX  
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Spaulding V;  
 XX  
 DR WPI; 2002-582343/62.  
 DR P-PSDB; ABP61800.  
 XX  
 PT Novel secreted or transmembrane protein and polynucleotide encoding the  
 PT protein, useful for diagnosis and treatment of neurological disorders,  
 PT cancer, autoimmune diseases, bone disorders and lung or liver fibrosis  
 XX  
 PS Claim 50; Page 113-114; 284pp; English.  
 XX  
 CC The invention relates to human secreted or transmembrane protein (I),  
 CC their fragments and is encoded by specific complementary deoxyribonucleic  
 CC acid (cDNA) inserts (II), where the protein is substantially free from  
 CC other mammalian proteins. (I) are useful for preventing, treating or  
 CC ameliorating a medical condition, especially immunological treatment or  
 CC prevention of tumours. (I) exhibits activity relating to angiogenesis,  
 CC cytokine, cell proliferation, cell differentiation, antiinflammatory,  
 CC stem cell growth factor activity and activin or inhibin-related  
 CC activities. (I) can be used to manipulate stem cells in culture to give  
 CC rise to neuroepithelial cells that can be used to augment or replace  
 CC cells damaged by illness, autoimmune disease, accidental damage or  
 CC genetic disorders. (I) induces the proliferation of neural cells and  
 CC regeneration of nerve and brain tissue and is useful for the treatment of  
 CC central and peripheral nervous system diseases and neuropathies, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis. (I) is involved in chemotactic or chemokinetic  
 CC activity, regulation of haematopoiesis and is useful for treating myeloid  
 CC and lymphoid cell disorders, platelet disorders such as thrombocytopaenia  
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
 CC tissue growth and in tissue repair, healing of burns, incisions, ulcers,  
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders or  
 CC periodontal disease. (I) is also useful for gut protection or  
 CC regeneration and treatment of lung or liver fibrosis, reperfusion injury  
 CC in various tissues, various immune deficiencies and disorders including  
 CC severe combined immunodeficiency (SCID), bacterial or fungal infections,  
 CC autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,  
 CC diabetes mellitus, myasthenia gravis, allergic reactions and conditions,  
 CC such as asthma or other respiratory problems. (II) is useful to express

CC recombinant protein, as markers for tissues in which the corresponding  
CC protein is preferentially expressed and in gene therapy. The present  
CC sequence is that of a polynucleotide of the invention.

XX Sequence 1851 BP, 531 A; 413 C; 438 G; 469 T; 0 other;

#### Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	0.0186	1851	10	0	0	0
Percent Similarity:	100.00%					
Best Local Similarity:	100.00%					
Query Match:	100.00%					
DB:	24					

US-09-745-763-36\_COPY\_231\_240 (1-10) x ABQ92016 (1-1851)

Oy 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
Db 789 ACAGCCTGTATTACGCTGGAGATGACGAA 818

#### RESULT 12

ID AAK94491 standard; cDNA; 1860 BP.

XX AAK94491;

DT 06-NOV-2001 (first entry)

XX Human full-length cDNA, SEQ ID NO: 3328.

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.

PN EP1130094-A2.

PD 05-SEP-2001.

PF 07-JUL-2000; 2000EP-0114089.

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI: 2001-524255/58.

DR P-PSDB: AAM93559.

PT 830 Primers useful for synthesizing full length cDNA clones and their

PT use in genetic manipulation -

XX Claim 8; SEQ ID NO 3328; 1380bp + sequence listing; English.

XX The invention relates to primers for synthesizing full length cDNA

XX clones. 830 cDNA molecules encoding a human protein have been

XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA

XX cDNA are useful for clarifying the function of the protein encoded by

XX the cDNA. The full length clones were obtained by construction of full

XX length enriched cDNA libraries that were synthesized by the oligo-capping

XX method. The primers enable the production of the full length cDNA easily

XX without any special methods. The present sequence is a full length

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	0.0187	1860	10	0	0	0
Percent Similarity:	100.00%					
Best Local Similarity:	100.00%					
Query Match:	100.00%					
DB:	22					

US-09-745-763-36\_COPY\_231\_240 (1-10) x AAK94491 (1-1860)

Oy 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
Db 819 ACAGCCTGTATTACGCTGGAGATGACGAA 848

#### RESULT 13

ID AAZ98034 standard; cDNA; 1863 BP.

XX AAZ98034;

DT 09-MAY-2000 (first entry)

XX Human secreted protein encoding nucleotide sequence SEQ ID NO:28.

XX Human; secreted protein; diagnosis; cytostatic; immunosuppressive;

XX antiinflammatory; nootropic; neuroprotective; antiallergic; cancer;

XX tumour; neurodegenerative disorder; developmental abnormality; allergy;

XX foetal deficiency; blood disorder; immune system disorder; arthritis;

XX autoimmune disease; hepatic disease; renal disease; inflammation;

XX Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis;

XX infection; AIDS; spinal cord injury; transplant rejection; diabetes;

XX aetna; sepsis; acne; psoriasis; cardiovascular disorder;

XX reproductive disorder; gastrointestinal disorder; respiratory disorder;

XX metabolic disorder; food additive; preservative; ss.

XX Homo sapiens.

PN WO200004140-A1.

PD 27-JAN-2000.

PF 14-JUL-1999; 99WO-US15849.

PR 15-JUL-1998; 98US-0092921.

PR 15-JUL-1998; 98US-0092922.

PR 15-JUL-1998; 98US-0092956.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Komatsoulis G, Duan RD, Rosen CA, Moore PA, Shi Y;

PI Lafleur DM, Ebner R, Olsen HS, Brewer LA, Florence KA, Young PE;

PI Mucenki M, Endress GA, Soppet DR;

DR WPI: 2000-161128/14.

DR P-PSDB: AAY87081.

PT New isolated human genes, useful for diagnosis and treatment of, e.g.

PT cancers, neurological or blood disorders -

XX Claim 1; Page 319; 494pp; English.

XX The polynucleotide sequences given in AAZ98017 to AAZ98108 encode the

XX human secreted proteins given in AAY87064 to AAY87223. Human secreted

protein can have activities based on the tissues and cells the genes are

expressed in. Examples of activities include: cytostatic; neuroprotective; and

immunosuppressive; antiinflammatory; nootropic; neuroprotective; and

antiallergic. The polynucleotides and their corresponding secreted

polypeptides are useful for preventing, treating or ameliorating medical

conditions, e.g. by protein or gene therapy. Also pathological conditions

can be diagnosed by determining the amount of the new polypeptides in a

sample or by determining the presence of mutations in the new

polynucleotides. Human secreted protein s and their polynucleotides can

be used for developing products for the diagnosis or treatment of cancer,

tumours, neurodegenerative disorders, developmental abnormalities and

CC foetal deficiencies, blood disorders, diseases of the immune system,  
 CC autoimmune diseases, hepatic and renal disease, inflammation,  
 CC Alzheimer's disease, behavioural disorders, schizophrenia,  
 CC osteoporosis, arthritis, infections, AIDS, spinal cord injuries,  
 CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,  
 CC cardiovascular disorders, reproductive disorders, gastrointestinal  
 CC disorders, respiratory disorders and metabolic disorders. The  
 CC proteins or polynucleotides can also be used as food additives or  
 CC preservatives. The proteins are also useful for identifying their  
 CC binding partners. AA298008 to AA298016 and AA87063 are sequence used in  
 CC the exemplification of the present invention.

XX Sequence 1863 BP; 533 A; 417 C; 443 G; 470 T; 0 other;

#### Alignment Scores:

Pred. No.:	Length:	1863
Score:	10.00	10
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
	21	Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AA298034 (1-1863)

Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
 Db 789 ACAGCCTGTATTACGGTGCAGATGCAGAA 818

RESULT 14  
 AAD11647  
 ID AAD11647 standard; cDNA; 1863 BP.

AC AAD11647;  
 XX 24-SEP-2001 (first entry)

XX Human secreted protein-encoding gene 18 cDNA clone HRACJ35, SEQ ID NO:28.

XX Human; secreted protein; proliferative disorder; cancer; tumour; asthma;  
 XX foetal abnormality; developmental abnormality; haematopoietic disorder;  
 XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 XX Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;  
 XX psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;  
 XX inflammation; neurological disorder; Alzheimer's disease; food additive;  
 XX angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;  
 XX pregnancy-related disorder; endocrine disorder; infection; wound healing;  
 XX cell culture; chemotaxis; vulnery; binding partner identification;  
 XX gene therapy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 99..1517  
 XX FT /\*tag= a  
 XX FT /product= "Human secreted protein precursor"  
 XX FT sig\_peptide 99..170  
 XX FT /\*tag= b  
 XX FT mat\_peptide 171..1514  
 XX FT /\*tag= c  
 XX FT /product= "Mature human secreted protein"

XX MO200151504-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001MO-US00911.

XX 13-JAN-2000; 2000US-0482273.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Komatsoulis GA, Duan DR, Rosen CA, Moore PA, Shi Y;  
 XX Lafleur DM, Olsen HS, Brewer LA, Florence KA, Young PE, Soppet DR;

PI Endress GA, Muscenski M, Ebner R;  
 XX WPI: 2001-425865/45.  
 DR P-PSDB; AA06058.

XX Isolated nucleic acid molecule encoding a human secreted protein is  
 PT used in preventing, treating or ameliorating a medical condition -

PS Claim 1; Page 686; 864pp; English.

XX AAD11630-AAD11721 represent cDNAs corresponding to 71 human secreted  
 CC protein genes, and AA06041-AA06132 represent the proteins they encode.  
 CC AA06133-AA06205 represent human secreted protein fragments.  
 CC The secreted proteins and their genes are useful for preventing, treating  
 CC or ameliorating medical conditions, e.g., by protein or gene therapy,  
 CC pathological conditions can be diagnosed by determining the amount of the  
 CC new protein in a sample or by determining the presence of mutations in  
 CC the new genes. Specific uses are described for each of the 71 genes,  
 CC based on the tissues in which they are most highly expressed, and include  
 CC developing products for the diagnosis or treatment of proliferative  
 CC disorders, cancer, tumours, foetal and developmental abnormalities,  
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune  
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,  
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),  
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,  
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,  
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,  
 CC pregnancy-related disorders, endocrine disorders, and infections. The  
 CC proteins can also be used to aid wound healing and epithelial cell  
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
 CC before transplantation, for supporting cell culture of primary tissues,  
 CC to regenerate tissues, to identify their cognate ligands or binding  
 CC partners, and in chemotaxis, and can be used as a food additive or a  
 CC preservative to modify storage properties. Antibodies specific for a  
 CC protein of the invention can be used in alleviating symptoms associated  
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,  
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).  
 CC The present sequence represents a human secreted protein-encoding cDNA of  
 CC the invention.

XX Sequence 1863 BP; 533 A; 417 C; 443 G; 470 T; 0 other;

#### Alignment Scores:

Pred. No.:	Length:	1863
Score:	10.00	Matches: 10
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
	22	Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AAD11647 (1-1863)

Qy 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
 Db 789 ACAGCCTGTATTACGGTGCAGATGCAGAA 818

RESULT 15  
 ABE69743  
 ID ABE69743 standard; cDNA; 1863 BP.

XX ABE69743;

XX 15-JUL-2002 (first entry)

XX Human secreted protein gene 18 #1.

XX Human; ss; gene; secreted protein; gene therapy; immunosuppressive;  
 XX antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac;  
 XX vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;  
 XX virucide; fungicide; opthalmological; autoimmune disease; neoplasm;  
 XX rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;  
 XX cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;  
 XX angiogenesis; nervous system disorder; Alzheimer's disease; infection;

KM ocular disorder; corneal infection; wound healing; skin aging;  
KM epithelial cell proliferation; food additive.

OS Homo sapiens.

PN WO200226931-A2.

XX 04-APR-2002.

PD 24-SEP-2001; 2001WO-US29871.

XX 25-SEP-2000; 2000US-234925P.

PR 12-JAN-2001; 2001WO-US00911.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Komatsoulis G, Duan DR, Rosen CA, Moore PA, Shi Y;  
PI Lafleur DM, Olsen H, Brewer LA, Florence KA, Young PE, Soppet DR;  
PI Endress GA, Mucenski M, Ebner R;

XX WPI: 2002-362489/39.

DR P-PSDB; ABG33880.

XX Novel 71 isolated secreted polypeptides and polynucleotides encoding

PT the polypeptides, useful for treating Huntington's disease, sepsis,  
PT meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,  
PT asthma

XX Claim 1; Page 1170; 1478pp; English.

XX The invention relates to an isolated nucleic acid molecule (or its

CC fragment, homologue complement or allelic variant) encoding a human

CC secreted protein (and its fragment, domain, epitope, variant, secreted

CC form and species variant). Also included are a recombinant vector

CC comprising the nucleic acid, a recombinant host cell comprising the

CC vector, an antibody against the secreted protein, a recombinant host cell

CC that expresses the secreted protein and a method of identifying a binding

CC partner of the secreted protein. The nucleic acid and protein are used to

CC prevent, diagnose, treat or ameliorate a medical condition in e.g.

CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep

CC for example autoimmune diseases e.g. rheumatoid arthritis,

CC hyperproliferative disorders e.g. neoplasms of the breast or liver,

CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders

CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.

CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and

CC ocular disorders e.g. corneal infection. Many other diseases and

CC disorders are listed in the specification. The polypeptides can also be

CC used to aid wound healing, to maintain organs before transplantation, for

CC skin aging due to sunburn, to maintain organs before transplantation, for

CC supporting cell culture of primary tissues, to regenerate tissues and in

CC chemotaxis. The polypeptides can also be used as a food additive or

CC preservative to increase or decrease storage capabilities. The present

CC sequence encodes a novel human secreted protein of the invention.

XX SQ Sequence 1863 BP; 533 A; 417 C; 443 G; 470 T; 0 other;

XX Alignment Scores:

XX Pred. No.: 0.0187

XX Score: 10.00

XX Percent Similarity: 100.00%

XX Best Local Similarity: 100.00%

XX Query Match: 100.00%

XX DB: 24

XX Gaps: 0

XX US-09-745-763-36\_COPY\_231\_240 (1-10) x ABK69743 (1-1863)

XX Oy 1 ThralaCysfIeThrValGluAspAlaGlu 10

XX Db 789 ACAGCCTGTATTCGTTGAGATGACGAA 818

Search completed: December 23, 2003, 12:39:26

Job time : 259 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 23, 2003, 12:00:30 ; Search time 2046 Seconds  
(without alignments)  
118.790 Million cell updates/sec

Title: US-09-745-763-36\_COPY\_231\_240  
Perfect score: 10  
Sequence: 1 TACTIVEDAE 10

Scoring table:  
OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues  
Word size: 1  
Total number of hits satisfying chosen parameters: 45557478

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Listing first 45 summaries

Command line parameters:  
-MODE=frame\_plus\_p2n.model -DEV=slp  
-O=/cgn2\_1/USPTO.spool.p/US09745763/runat\_23122003\_120024\_20097/app\_query.fasta\_1.199  
-DB=EST -QFMT=fastap -SUFFIX=olip2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pico  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09745763@CNCN\_1.1.3549@runat\_23122003\_120024\_20097 -NCPU=6 -ICPU=3  
-NO\_MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPILOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :  
EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estnu: \*  
5: em\_estrov: \*  
6: em\_estrpl: \*  
7: em\_estro: \*  
8: em\_hic: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_est3: \*  
12: gb\_est4: \*  
13: gb\_est5: \*  
14: gb\_estfun: \*  
15: em\_estom: \*  
16: em\_estom: \*  
17: em\_ges\_hum: \*  
18: em\_ges\_hum: \*  
19: em\_ges\_hum: \*  
20: em\_ges\_vrt: \*  
21: em\_ges\_fun: \*  
22: em\_ges\_mam: \*  
23: em\_ges\_mus: \*  
24: em\_ges\_pro: \*  
25: em\_ges\_rod: \*  
26: em\_ges\_png: \*  
27: em\_ges\_vr1: \*  
28: gb\_ges1: \*

29: gb\_ges2: \*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	174	9	AA790960
2	10	100.0	296	9	AA790960
3	10	100.0	313	10	AA329616
4	10	100.0	314	13	BE833868
5	10	100.0	317	10	BE833878
6	10	100.0	320	10	BE833882
7	10	100.0	334	10	BE833866
8	10	100.0	362	9	AA790981
9	10	100.0	442	9	AI021522
10	10	100.0	443	9	AA634903
11	10	100.0	443	9	AA634903
12	10	100.0	463	9	AA631136
13	10	100.0	463	9	AI050369
14	10	100.0	475	9	AA105255
15	10	100.0	504	9	AA452391
16	10	100.0	524	13	BU696863
17	10	100.0	528	13	BU694506
18	10	100.0	544	10	AA952474
19	10	100.0	576	12	BM256759
20	10	100.0	592	13	BU695545
21	10	100.0	637	13	BO564473
22	10	100.0	650	10	BG432644
23	10	100.0	653	10	BE218907
24	10	100.0	662	14	BY747978
25	10	100.0	676	9	AA796802
26	10	100.0	677	10	BE670618
27	10	100.0	707	14	CD366462
28	10	100.0	739	14	CB958693
29	10	100.0	752	14	W28330
30	10	100.0	793	14	CB234306
31	10	100.0	794	14	CD356404
32	10	100.0	804	14	CD352906
33	10	100.0	813	14	CD519131
34	10	100.0	866	13	BU146905
35	10	100.0	902	10	BG751497
36	10	100.0	909	13	BQ878966
37	10	100.0	919	13	EX335995
38	10	100.0	926	13	BO938234
39	10	100.0	998	13	BX460463
40	10	100.0	1012	13	BX416896
41	10	100.0	1024	11	BC012019
42	10	100.0	1038	13	BX355940
43	10	100.0	1050	13	BX439467
44	10	100.0	1739	11	AK032972
45	10	100.0	1805	11	AK075686

ALIGNMENTS

RESULT 1	AA790960	174 bp	mRNA	linear	EST 06-FEB-1998
LOCUS	AA790960				
DEFINITION	AA790960				
ACCESSION	AA790960				
VERSION	AA790960.1				
KEYWORDS	GI:2851080				
SOURCE	EST				
ORGANISM	Mus musculus (house mouse)				
REFERENCE	1 (bases 1 to 174)				

AUTHORS	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gessel, S., Kincade, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellendberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.			
TITLE	The WashU-HHMI Mouse EST Project			
JOURNAL	Unpublished			
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.wustl.edu This clone is available royalty-free through LINDA; contact the IMAGE Consortium (info@image.lindl.gov) for further information. Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 82.			
FEATURES	Source 1.174 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:124312" /sex="male" /tissue_type="mammary gland" /dev_stage="4 weeks" /lab_host="DH10B" /clone_lib="Soares_mammary_gland_NbMNG" /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."			
BASE COUNT	46 a 42 c 41 g 44 t 1 others			
ORIGIN				
Alignment Scores:				
Pred. No.:	0.00216	Length:	174	
Score:	10.00	Matches:	10	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	9	Gaps:	0	
US-09-745-763-36_COPY_231_240 (1-10) x AA790960 (1-174)				
CY	1	ThralaCysIleThValGluAspAlaGlu 10		
LOCUS	EST313245	Embryo, 12 week II Homo sapiens cDNA 5' end, mRNA		
Db	118	ACAGCCTGTATCACAGTAGAAGATGCAGAA 147		
RESULT 2				
AA329616				
LOCUS	AA329616	296 bp	mRNA	linear
DEFINITION	EST 20-APR-1997			
ACCESSION	AA329616			
VERSION	AA329616.1 GI:1981858			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Mammalia, Eutheria, Primates, Catarrhini, Homnidae, Homo.			
AUTHORS	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult			

C. J., Lee N.H., Kitzness E.F., Weinstein K.G., Gocayne J.D., White  
'O', Sutton G., Blake J.A., Brandon R.C., Man-Wei C., Clayton R.A.,  
Cline T.R., Cotton M.D., Earle-Hughes D., Fine L.D., Fitzgerald  
'L.M., Fitzhugh W.M., Fritchman J.L., Georgagen N.S., Glodet A.,  
Gnehm C.L., Hanna M.C., Hedblom E., Hinkle P.S.Jr., Kelley J.M.,  
Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M.,  
Moreno-Palancas R.F., McDonald L.A., Nguyen D.T., Pelligrino S.M.,  
Phillips C.A., Ryder S.E., Scott J.L., Saudak D.M., Shirley R.,  
Small K.V., Spriggs T.A., Uterbeck T.R., Weidman J.F., Li Y.,  
Bednarik D.P., Cao L., Cepede M.A., Coleman T.A., Collins E.J.,  
Dinke D., Feng D.F., Ferlie A., Fischer C., Hastings G.A., He W.W.,  
Hu J.S., Greene J.M., Gruber J., Hudson P., Kim A.K., Kozak D.L.,  
Kunsch C., Hungjun J., Li H., Weisner P.S., Olsen H., Raymond L.,  
Wei Y.F., Wang T., Xu C., Yu G.L., Ruben S.M., Dillon P.J., Fannon  
'M.R., Rosen C.A., Haefeltine W.A., Fields C., Fraser C.M. and  
Venier J.C.  
Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of cDNA sequence  
Nature 377 (6547 Suppl), 3-174 (1995)  
96026280  
7566098  
Other ESTs: THC171697  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..296  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/db\_xref="taxon:9606"  
/dev\_stage="embryo, 12 wks"  
/clone\_id="Embryo, 12 week II"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
XhoI"  
BASE COUNT 84 a 62 c 79 g 69 t 2 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 0.00374 Length: 296  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-745-763-36\_COPY\_231\_240 (1-10) x AA329616 (1-296)  
QY 1 Thra1aCys11ethrVa1giuaspAla1g1u 10  
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61 ACAGCCTGTATTACGTGGAAGATGACGAGA 90  
RESULT 3  
BE833868 313 bp mRNA linear EST 22-SEP-2000  
LOCUS BE833868  
DEFINITION RC6-OT0076-220500-012-B07 OT0076 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE833868  
VERSION BE833868.1 GI:10266246  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 313)  
Das Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,



**TITLE**  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.U.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

**JOURNAL**  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

**MEDLINE**  
20202663

**PUBMED**  
10737800

**COMMENT**  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-27049922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml.pl?file=RC6-OT0076-220  
500-012-B07&ts=2000-05-22&ts=1)  
Seq primer: puc 18 forward  
High quality sequence start: 19  
High quality sequence stop: 313.  
Location/Qualifiers

**FEATURES**  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="adult"  
/clone\_lib="OT0076"  
/note="Organ: ovary; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
, 716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

**BASE COUNT**  
70 a 80 c 76 g 87 t

**ORIGIN**

**Alignment Scores:**  
Pred. No.: 0.00397 Length: 313  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x BE833868 (1-313)

**Qy**  
1 ThralAcysileThrValGluAspAlaGlu 10  
|||||  
171 ACAGCCTGTATTACGTGGAAGATGCAGAA 142

**Db**

**RESULT 4**  
BX091504 314 bp mRNA linear EST 23-JAN-2003  
BX091504 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone  
IMAGE:796263, mRNA sequence.  
BX091504.1 GI:27826297  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 314)  
Ebert,L., Hell,O., Hennig,S., Neubert,P., Patsch,E., Peters,M.,  
Radejof,U., Schneider,D. and Korn,B.

**REFERENCE**  
1 (bases 1 to 314)  
Ebert,L., Hell,O., Hennig,S., Neubert,P., Patsch,E., Peters,M.,  
Radejof,U., Schneider,D. and Korn,B.

**AUTHORS**  
Human Unigeneset - RZPD3

**TITLE**  
Unpublished

**JOURNAL**

**COMMENT**  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD: IMAGE9980161963.  
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No. 972)  
http://www.rzpd.de/ClonCards/cgi-  
bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r. Primer sequence: TTTCACACAGGAAGACGTATGAC.  
Location/Qualifiers

**FEATURES**  
source  
1..314  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE9980161963 ; IMAGE:796263"  
/dev\_stage="8-9 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Soares total fetus Nb2HF8 9w"  
/note="Vector: pRT3D-pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from pooled 8-9 week  
(total) fetus material with a Not I - oligo(dt) primer (5'  
TGTTCCATCTGATGAGCGGCGCGCTTATTTTATTTT 3').  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pRT3 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

**BASE COUNT**  
88 a 64 c 87 g 73 t

**ORIGIN**

**Alignment Scores:**  
Pred. No.: 0.00398 Length: 314  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x BX091504 (1-314)

**Qy**  
1 ThralAcysileThrValGluAspAlaGlu 10  
|||||  
35 ACAGCCTGTATTACGTGGAAGATGCAGAA 64

**Db**

**RESULT 5**  
BE833878 317 bp mRNA linear EST 22-SEP-2000  
RC6-OT0076-220500-012-E04 OT0076 Homo sapiens cDNA, mRNA sequence.  
BE833878  
BE833878.1 GI:10266256  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 317)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.U.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

**REFERENCE**  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

**AUTHORS**

**TITLE**

**JOURNAL**

**MEDLINE** 20202663  
**PUBMED** 10737800  
**COMMENT** Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6-OT0076-220500-012-504&ct3=2000-05-22&ct4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 11  
 High quality sequence stop: 317.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="OT0076"  
 /note="Organ: ovary; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
**BASE COUNT** 71 a 84 c 76 g 86 t  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 0.00402 Length: 317  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0  
 US-09-745-763-36\_COPY\_231\_240 (1-10) x BE833878 (1-317)  
**Qy** 1 ThrAlaCysIleThrValGluAapAlaGlu 10  
 |||||||  
**Db** 175 ACAGCCTGTATACGCTGAGATGCAGAA 146  
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**RESULT 6** BE833882 320 bp mRNA linear EST 22-SEP-2000  
**LOCUS** RC6-OT0076-220500-012-F03 OT0076 Homo sapiens cDNA, mRNA sequence.  
**DEFINITION** BE833882  
**ACCESSION** BE833882.1 GI:10266260  
**VERSION** EST.  
**KEYWORDS** Homo sapiens (human)  
**SOURCE** Homo sapiens  
**ORGANISM** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE** 1 (bases 1 to 320)  
**AUTHORS** Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
**MEDLINE** 20202663  
**PUBMED** 10737800  
**COMMENT** Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6-OT0076-220500-012-F03&ct3=2000-05-22&ct4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 10  
 High quality sequence stop: 320.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="OT0076"  
 /note="Organ: ovary; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
**BASE COUNT** 73 a 83 c 75 g 89 t  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 0.00406 Length: 320  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0  
 US-09-745-763-36\_COPY\_231\_240 (1-10) x BE833882 (1-320)  
**Qy** 1 ThrAlaCysIleThrValGluAapAlaGlu 10  
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**Db** 178 ACAGCCTGTATACGCTGAGATGCAGAA 149  
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**RESULT 7** BE833866 334 bp mRNA linear EST 22-SEP-2000  
**LOCUS** RC6-OT0076-220500-012-A10 OT0076 Homo sapiens cDNA, mRNA sequence.  
**DEFINITION** BE833866  
**ACCESSION** BE833866  
**VERSION** BE833866.1 GI:10266244  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**ORGANISM** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE** 1 (bases 1 to 334)  
**AUTHORS** Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
**MEDLINE** 20202663  
**PUBMED** 10737800  
**COMMENT** Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922

Fax: +55-11-2707001  
 Email: [aslism@ludwig.org.br](mailto:aslism@ludwig.org.br)  
 This sequence was derived from the PAPBP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
<http://www.ludwig.org.br/scripts/gethtml2.pl?r1=kt2=RC6-OT0076-220500-012-1A0&r3=2000-05-22&r4=1>  
 Seq primer: puc.18 forward  
 High quality sequence start: 38  
 High quality sequence stop: 334.  
 Location/Qualifiers

**FEATURES**

**SOURCE**

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="OT0076"
/note="Organ: ovary; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 1997, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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BASE COUNT	77 a	86 c	80 g	91 t
ORIGIN				

Alignment Scores:

Pred. No.:	0.00425	length:	33
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-745-763-36\_COPY\_231\_240 (1-10) X BE833866 (1-334)

**Dy**      1 ThrIACysileThrValGluaspalaglu 10  
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**Db**    192 ACAGCCTGTATTACGGTGAAGATGCAGAA 167

RESULT	8
AA790981	
LOCUS	
DEFINITION	
AA790981	362 bp mRNA linear EST 06-FEB-1998
vW20905.t1 Scaree mammary gland_NBMKG Mus musculus cDNA clone	
IMAGE:1244408 5'	mRNA sequence.

ACCESSION	AA790981
VERSION	AA790981.1
KEYWORDS	EST.

SOURCE ORGANISM	Mus musculus (house mouse) Mus musculus
1	1
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100	100

REFERENCE  
AUTHORS

1 (bases 1 to 362)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubouque, T.,

Euarchyotia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Gaebel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE	The WashU-HIMI Mouse EST Project
JOURNAL	Unpublished
COMMENT	Contact: Marra M/Mouse EST Project

WashU-HIMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

**Tel: 314 286 1800**  
**Fax: 314 286 1810**  
**Email: [mouseest@watson.wustl.edu](mailto:mouseest@watson.wustl.edu)**

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information  
MCT-658096

Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 321.

## FEATURES

**source**

```

1.362
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1244408"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NbWNG"
/notes="Organ: mammary gland; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (27) primer [5'
TGTTCACATCTGTAAGTGGAGGCGCCGCAATGCTTTTTTTTTTTTTTTTTT
T 3'] ; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRTT3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

```

BASE COUNT	97 a	74 c	97 g	93 t	1 others
ORIGIN					

Alignment Scores:

Pred. No.:	0.00462	Length:	36
Score:	10.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-745-763-36 COPY\_231\_240 (1-10) X AA790981 (1-362)

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QY      1 ThrAlacysIleThrValGluAspAlaglu 10
        |||||
DB     118 ACAGCCTGTATCACAGTAGAAGATGCAGAA 147
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RESULT 9	LOCUS	DEFINITION
A1021522	442 bp mRNA	linear EST 16-JUN-1998
U021522		
AB09a06.r1 Soares_mammary_gland_NbMNG Mus musculus CDNA clone		
IMAGE:1366450 5', mRNA sequence.		

ACCESSION	AI021522
VERSION	AI021522.1
KEYWORDS	EST.

SOURCE ORGANISM	Mus musculus (house mouse) Mus musculus
1	
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99	
100	

REFERENCE  
AUTHORS

1 (bases 1 to 442)

Matta, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognath; Muridae; Murinae; Mus.

Getsele, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Streptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE	The WashU-HHMI Mouse EST Project
JOURNAL	Unpublished
COMMENT	Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314.772.3100

Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [monroe@atcon.net](mailto:monroe@atcon.net)

EMAIL: [info@image.jnl.edu](mailto:info@image.jnl.edu)  
<http://image.jnl.edu>  
 This clone is available royalty-free through LNL ; contact the  
 IMAGE Consortium ([info@image.jnl.edu](mailto:info@image.jnl.edu)) for further information.

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop:

**FEATURES**

/organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1366450"  
 /sex="male"  
 /tissue\_type="mammary gland"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"  
 /clone\_11b="Soares\_mammary\_gland NbMNG"  
 /note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia)  
 ) with a modified polylinker; Site 1: Not I; Site 2: Eco  
 RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
 primer [5',  
 TGGTACCACTGAACTGGAGCGCGCGCAATGCTTTTCTTTTCTTTTCTTTT  
 T 3']; double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pT73 vector.  
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
 constructed and normalized by Bento Soares and W. Fatima  
 Bonaldi."

BASE COUNT 122 a 85 c 124 g 111 t  
 ORIGIN

Alignment Scores:  
 Pred. NO.:  
 Score: 0.00568 Length: 442  
 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x A1021522 (1-442)

Oy 1 Thr1aCys11eThr1va1GuASP1a1a1u 10  
 |||||  
 Db 41 ACAGCCTGATCAGCTAGAGATGTCAGAA 70

RESULT 10 443 bp mRNA linear EST 06-MAR-1998  
 LOCUS AA634903  
 DEFINITION IMAGE:842076 5', mRNA sequence.  
 ACCESSION AA634903  
 VERSION AA634903.1 GI:2558117  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 443)  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,  
 Kitzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Merra, M., Martin  
 , J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
 White, Y., Wyllie, T., Waterston, R. and Wilson, R.  
 Washu-NCI human EST Project  
 Unpublished  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: east@wustl.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 1304 Std Error: 0.00  
 Seq primer: -28m13 rev1 ET from Amersham  
 High quality sequence stop: 442.  
 Location/Qualifiers  
 1..443  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"

FEATURES  
 source

TITLE  
 JOURNAL  
 COMMENT

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/clone="IMAGE:842076"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_1lb="Stratagene lung (#937210)"
/notes="Organ: lung; Vector: pBluescript SK-; Site 1: EcoRI
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR
Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3'
adaptor sequence: 5' CTCGAGCTTTT TTTT TTTT 3'."
BASE COUNT      112 a      95 c      126 g      109 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:      0.00569      Length:      443
Score:          10.00      Matches:      10
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:          9      Gaps:      0

US-09-745-763-36_COPY_231_240 (1-10) x AA634903 (1-443)
Cy      1 ThrAACysIethrValGluASPAlaGlu 10
|||||
107 ACACCTGTATTACGTGTGAAGATGCAGAA 136

RESULT 11
LOCUS      AA461136      443 bp      mRNA      linear      EST 09-JUN-1997
DEFINITION IMAGE:796263 5', mRNA sequence.
ACCESSION AA461136
VERSION AA461136.1 GI:2186256
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 443)
Hillier L., Allen M., Bowles J., Dubuque T., Geisell G., Joet S.,
Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B.,
Schlenderberg K., Steptoe M., Tan F., Theising R., White Y., Wyllie
T., Waterston R. and Wilson R.
WashU-Merck EST Project 1997
Unpublished
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through HUNT; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 416.
Location/Qualifiers
1..443
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:6040267"
/db_xref="taxon:9606"
/clone="IMAGE:796263"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/clone_1lb="soares_total_fetus_Nb2HF8_9w"
/notes="Vector: pRT7D-Poc (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(fetal) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAATGGAGCGGCGCTTATTTT TTTT TTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I

```



## Alignment Scores:

Pred. No.: 0.00612 Length: 475  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AA452391 (1-475)

Qy 1 ThralAcyllethrrValGluaspAlaGlu 10  
 Db 248 ACAGCCTGTATCAGTGAAGATGCAGAA 277

RESULT 14  
 AA452391 504 bp mRNA linear EST 05-JUN-1997  
 LOCUS 2249C10.t1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone  
 DEFINITION IMAGE:787890 5', mRNA sequence.

ACCESSION AA452391  
 VERSION AA452391.1 GI:2166060  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM

REFERENCE  
 AUTHORS Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE  
 JOURNAL  
 COMMENT  
 Contact: Wilson R.  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -28m13 rev2 ET from Amersham  
 High quality sequence stop: 472.

## FEATURES

source  
 Location/Qualifiers  
 1..504

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:5985507"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:787890"  
 /dev\_stage="8-9 weeks"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares\_total\_fetus\_Nb2HF8\_9w"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was prepared from mRNA obtained from pooled 8-9 week  
 (total) fetus material with a Not I - oligo(dT) primer [5'  
 TGTTCACATCTGAAGTGGAGCGCCGCTTAATTTTITTTTITTTT 3']  
 Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 136 a 107 c 141 g 120 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 0.00651 Length: 504  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x AA452391 (1-504)

Qy 1 ThralAcyllethrrValGluaspAlaGlu 10  
 Db 11 ACAGCCTGTATCAGTGAAGATGCAGAA 40

RESULT 15  
 BU696863 524 bp mRNA linear EST 09-OCT-2002  
 LOCUS LU21n13969T7 Hematopoietic Stem Cell Subtracted Library Mus  
 DEFINITION musculus cDNA 5' similar to hematopoietic lineage switch 2, mRNA  
 sequence.

ACCESSION BU696863  
 VERSION BU696863.1 GI:23607807  
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
 ORGANISM

REFERENCE  
 AUTHORS

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 Contact: Lemischka, Ihor R.  
 Department of Molecular Biology  
 Princeton University  
 Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA  
 Tel: 609 258 2838  
 Fax: 609 258 2759  
 Email: ilemischka@molbio.princeton.edu  
 These ESTs are derived from a subtracted cDNA library enriched for  
 gene products expressed in day 14-14.5 fetal liver hematopoietic  
 stem cells defined as Lineages/10, AA4.1pos, ckitpos, Ly6A/E  
 (Sca-1)pos  
 Seq primer: M13Reverse or T7.

## FEATURES

source  
 Location/Qualifiers  
 1..524

/organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57Bl/6J"  
 /db\_xref="taxon:10090"  
 /db\_xref="Hematopoietic"  
 /cell\_type="Stem Cells; Lineages/10, AA4.1pos, ckitpos,  
 Ly6A/E (Sca-1)pos"  
 /dev\_stage="Embryonic day 14-14.5"  
 /lab\_host="DH10B"  
 /clone\_lib="Hematopoietic Stem Cell Subtracted Library"  
 /note="Organ: Fetal Liver; Vector: Sport 1, Site 1: Sal I;  
 Site 2: Not I; Two directionally cloned cDNA libraries  
 were made from fetal liver hematopoietic stem cells  
 enriched to be Lineages/10, AA4.1pos, ckitpos, Ly6A/E  
 (Sca-1)pos called Scapos and from AA4.1neg fetal liver  
 cells. Subtractive hybridization was performed by  
 hybridization of the target, Scapos, single stranded cDNA  
 library in pSport1 to biotinylated RNA transcribed from  
 the driver, AA4.1neg cDNA library in pSport2 with inserts  
 cloned in the complementary orientation. For detailed  
 protocols and additional information please see our  
 website at <http://stemcell.princeton.edu>. "

BASE COUNT 146 a 110 c 140 g 125 t 3 others  
 ORIGIN

## Alignment Scores:

Pred. No.: 0.00678 Length: 524  
 Score: 10.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x BU696863 (1-524)

QY 1 ThrAlaCysrIleThrValGluAspAlaGlu 10  
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Db 353 ACAGCCTGTATCACTAGAGATGCAGAA 382

Search completed: December 23, 2003, 12:34:58  
Job time : 2050 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 23, 2003, 12:00:30 ; Search time 74 Seconds  
(without alignments)  
59.646 Million cell updates/sec

Title: US-09-745-763-36\_COPY\_231\_240  
Perfect score: 10  
Sequence: 1 FACITVEDAE 10

Scoring table:  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1128671

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+g2n.model -DEV=x1p  
-Q=/cgn2\_1/USFTO.spool\_p/US09745763/runat\_23122003\_120024\_20116/app.query.fasta\_1.139  
-DB=Issued\_Patents\_NA -OPMT=fastap -SUFFIX=olip2n.rml -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09745763@cgn2\_1.1\_103@runat\_23122003\_120024\_20116 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6  
-Fgapext=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
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3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	1134	4	US-09-482-273-95
2	10	100.0	1863	4	US-09-482-273-28
3	6	60.0	536	3	US-08-714-918-57
4	6	60.0	536	3	US-09-265-315-57
5	6	60.0	536	3	US-09-265-315-57
6	6	60.0	536	3	US-09-265-315-57
7	6	60.0	1021	3	US-08-714-918-70
8	6	60.0	1021	3	US-09-265-315-70
9	6	60.0	1021	3	US-09-265-315-70
10	6	60.0	1021	3	US-09-265-315-70
11	6	60.0	1056	4	US-09-252-991A-14680
12	6	60.0	1595	4	US-09-461-325-17

13	6	60.0	1650	4	US-09-328-352-1770	Sequence 1770, Ap
14	6	60.0	1968	4	US-09-252-991A-15074	Sequence 15074, A
15	6	60.0	2585	2	US-08-579-777A-1	Sequence 1, Appl1
16	6	60.0	3206	1	US-08-373-134D-1	Sequence 1, Appl1
17	6	60.0	3206	2	US-09-114-637-1	Sequence 1, Appl1
18	6	60.0	3900	4	US-09-252-991A-14550	Sequence 14550, A
19	6	60.0	5115	3	US-08-348-518C-3	Sequence 3, Appl1
20	6	60.0	5115	3	US-08-476-509B-3	Sequence 3, Appl1
21	6	60.0	7042	3	US-09-092-508-1	Sequence 1, Appl1
22	6	60.0	7042	4	US-09-435-115-1	Sequence 1, Appl1
23	6	60.0	7042	4	US-09-098-310-1	Sequence 1, Appl1
24	6	60.0	7042	4	US-09-590-364-21	Sequence 21, Appl1
25	6	60.0	7075	3	US-09-092-508-15	Sequence 15, Appl1
26	6	60.0	7075	4	US-09-435-115-15	Sequence 15, Appl1
27	5	50.0	20	2	US-08-651-692-36	Sequence 36, Appl1
28	5	50.0	25	3	US-08-879-941-6	Sequence 6, Appl1
29	5	50.0	25	4	US-09-747-116-6	Sequence 6, Appl1
30	5	50.0	47	4	US-09-422-978-1729	Sequence 1729, Ap
31	5	50.0	147	3	US-09-020-956-57	Sequence 57, Appl1
32	5	50.0	147	3	US-09-030-607-57	Sequence 57, Appl1
33	5	50.0	147	4	US-09-352-616A-57	Sequence 57, Appl1
34	5	50.0	147	4	US-09-352-616A-57	Sequence 57, Appl1
35	5	50.0	168	4	US-09-232-149A-57	Sequence 117, App
36	5	50.0	168	4	US-09-702-705-117	Sequence 117, App
37	5	50.0	168	4	US-09-736-457-117	Sequence 1437, Ap
38	5	50.0	171	4	US-09-702-705-1437	Sequence 1437, Ap
39	5	50.0	171	4	US-09-736-457-1437	Sequence 1437, Ap
40	5	50.0	213	2	US-08-727-688-3	Sequence 3, Appl1
41	5	50.0	214	2	US-08-727-688-2	Sequence 2, Appl1
42	5	50.0	258	4	US-09-134-001C-1695	Sequence 1695, Ap
43	5	50.0	264	1	US-08-700-575-24	Sequence 24, Appl1
44	5	50.0	269	4	US-09-016-434-78	Sequence 78, Appl1
45	5	50.0	271	4	US-09-506-729-15	Sequence 15, Appl1

## ALIGNMENTS

### RESULT 1

US-09-482-273-95  
Sequence 95, Application US/09482273  
Patent No. 6534631  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 71 Human Secreted Proteins  
FILE REFERENCE: P2030P1  
CURRENT APPLICATION NUMBER: US/09/482,273  
CURRENT FILING DATE: 2000-01-13  
EARLIER APPLICATION NUMBER: PCT/US99/15849  
EARLIER FILING DATE: 1999-07-14  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/092,922  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/092,956  
EARLIER FILING DATE: 1998-07-15  
NUMBER OF SEQ ID NOS: 267  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 95  
LENGTH: 1134  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-482-273-95

### Alignment Scores:

Pred. No.: 0.00194  
Score: 10.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 4  
Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-482-273-95 (1-1134)

QY 1 ThrAlAcysilethrValGluAspAlaGlu 10  
| | | | | | | | | | | | | | | | | | | | | |  
Db 61 ACAGCCTGTATTACGGTGAAGATGACGAA 90

RESULT 2  
US-09-482-273-28  
Sequence 28, Application US/09482273  
Patent No. 6534631  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 71 Human Secreted Proteins  
FILE REFERENCE: P2030P1  
CURRENT APPLICATION NUMBER: US/09/482, 273  
CURRENT FILING DATE: 2000-01-13  
EARLIER APPLICATION NUMBER: PCT/US99/15849  
EARLIER FILING DATE: 1998-07-14  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/092,922  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/092,956  
EARLIER FILING DATE: 1998-07-15  
NUMBER OF SEQ ID NOS: 267  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 28  
LENGTH: 1863  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-482-273-28

Alignment Scores:  
Pred. No.: 0.00297 Length: 1863  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-482-273-28 (1-1863)

QY 1 ThrAlAcysilethrValGluAspAlaGlu 10  
| | | | | | | | | | | | | | | | | | | | | |  
Db 789 ACAGCCTGTATTACGGTGAAGATGACGAA 818

RESULT 3  
US-08-714-918-57/c  
Sequence 57, Application US/08714918  
Patent No. 6037123  
GENERAL INFORMATION:  
APPLICANT: Benton, Bret  
APPLICANT: Lee, Vang  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmid, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL  
TITLE OF INVENTION: TARGET GENES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/714,918  
FILING DATE: September 13, 1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 222/005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 536 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-714-918-57

Alignment Scores:  
Pred. No.: 41.6 Length: 536  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 3 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-08-714-918-57 (1-536)

QY 5 ThrValGluAspAlaGlu 10  
| | | | | | | | | | | | | | | | | | | | | |  
Db 254 ACTGTAGAGATGCTGAA 237

RESULT 4  
US-09-265-315-57/c  
Sequence 57, Application US/09265315  
Patent No. 6187541  
GENERAL INFORMATION:  
APPLICANT: Benton, Bret  
APPLICANT: Lee, Vang J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmid, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
TITLE OF INVENTION: TARGET GENES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
FILING DATE: March 9, 1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 536 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-265-315-57

Alignment Scores:  
Pred. No.: 41.6 Length: 536  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 3 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-265-315-57 (1-536)

QY 5 ThValGluApPaGlu 10  
Db 254 ACTGTAGAGATGCTGAA 237

RESULT 5  
US-09-265-315-57/c  
Sequence 57, Application US/09265315  
Patent No. 6187541  
GENERAL INFORMATION:  
APPLICANT: Benton, Bret  
APPLICANT: Lee, Ying J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmidt, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/265,315  
FILING DATE: March 9, 1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/714,918  
FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 536 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-265-315-57

Alignment Scores:  
Pred. No.: 41.6 Length: 536  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 3 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-265-315-57 (1-536)

QY 5 ThValGluApPaGlu 10  
Db 254 ACTGTAGAGATGCTGAA 237

RESULT 6  
US-09-266-417-57/c  
Sequence 57, Application US/09266417  
Patent No. 6228588  
GENERAL INFORMATION:  
APPLICANT: Benton, Bret  
APPLICANT: Lee, Ying J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmidt, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/266,417  
FILING DATE: March 9, 1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/714,918  
FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/248  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 536 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-266-417-57

Alignment Scores:  
Pred. No.: 41.6 Length: 536  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 3 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-266-417-57 (1-536)

OY 5 ThvAlGluAaPaLaglu 10  
Db 254 ACTGTAGAGATGCTGAA 237

RESULT 7  
US-08-714-918-70/c  
Sequence 70, Application US/08714918  
Patent No. 6037123

GENERAL INFORMATION:  
APPLICANT: Benton, Bret  
APPLICANT: Lee, Vang  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmid, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL  
TITLE OF INVENTION: TARGET GENES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/714,918  
FILING DATE: September 13, 1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 222/005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1021 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-714-918-70

Alignment Scores:  
Pred. No.: 72.5 Length: 1021  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 3 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-08-714-918-70 (1-1021)

OY 5 ThvAlGluAaPaLaglu 10  
Db 93 ACTGTAGAGATGCTGAA 76

RESULT 8  
US-09-265-315-70/c  
Sequence 70, Application US/09265315  
Patent No. 6187541

GENERAL INFORMATION:  
APPLICANT: Benton, Bret  
APPLICANT: Lee, Vang J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmid, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/265,315  
FILING DATE: March 9, 1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/714,918  
FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1021 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-265-315-70

Alignment Scores:  
Pred. No.: 72.5  
Score: 6.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 60.00%  
DB: 3

Length: 1021  
Matches: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-265-315-70 (1-1021)

QY 5 ThYvAlGluAspAlaGlu 10  
DB 93 ACTGTAGAGATGCTGAA 76

RESULT 9  
US-09-265-315-70/C  
Sequence 70, Application US/09265315  
Patent No. 6187541  
GENERAL INFORMATION:  
APPLICANT: Benton, Bret  
APPLICANT: Lee, Ying J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmidt, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
NUMBER OF INVENTION: TARGET GENES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/265,315  
FILING DATE: March 9, 1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/714,918  
FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1021 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
US-09-265-315-70

Alignment Scores:  
Pred. No.: 72.5  
Score: 6.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 60.00%  
DB: 3

Length: 1021  
Matches: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-265-315-70 (1-1021)

QY 5 ThYvAlGluAspAlaGlu 10  
DB 93 ACTGTAGAGATGCTGAA 76

RESULT 10  
US-09-266-417-70/C  
Sequence 70, Application US/09266417  
Patent No. 6228588  
GENERAL INFORMATION:  
APPLICANT: Benton, Bret  
APPLICANT: Lee, Ying J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmidt, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
NUMBER OF INVENTION: TARGET GENES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/266,417  
FILING DATE: March 9, 1999  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/714,918  
FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/248  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1021 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-266-417-70

## Alignment Scores:

Pred. No.: 72.5 Length: 1021  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 3 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-266-417-70 (1-1021)

QY 5 ThrvAlGuaaPaAlaGlu 10  
Db 93 ACTGTAGAGATGCTGAA 76

## RESULT 11

US-09-252-991A-14680  
Sequence 14680, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 14680  
LENGTH: 1056  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-14680

## Alignment Scores:

Pred. No.: 74.6 Length: 1056  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 4 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-252-991A-14680 (1-1056)

QY 4 1leThrvAlGuaaPaAla 9  
Db 265 ATCACGTCGAGATGCC 282

## RESULT 12

US-09-461-325-17/C  
Sequence 17, Application US/09461325A  
Patent No. 6475753  
GENERAL INFORMATION:

APPLICANT: Ruben et al.  
TITLE OF INVENTION: 94 Human Secreted Proteins  
FILE REFERENCE: P202991  
CURRENT APPLICATION NUMBER: US/09/461,325A  
CURRENT FILING DATE: 1999-12-14  
EARLIER APPLICATION NUMBER: PCT/US99/13418  
EARLIER FILING DATE: 1999-06-15  
EARLIER APPLICATION NUMBER: 60/089,507  
EARLIER FILING DATE: 1998-06-16  
EARLIER APPLICATION NUMBER: 60/089,508  
EARLIER FILING DATE: 1998-06-16  
EARLIER APPLICATION NUMBER: 60/089,509  
EARLIER FILING DATE: 1998-06-16  
EARLIER APPLICATION NUMBER: 60/089,510  
EARLIER FILING DATE: 1998-06-16  
EARLIER APPLICATION NUMBER: 60/090,112  
EARLIER FILING DATE: 1998-06-22  
EARLIER APPLICATION NUMBER: 60/090,113

EARLIER FILING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 532  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 1595  
TYPE: DNA  
ORGANISM: Homo sapiens

US-09-461-325-17

## Alignment Scores:

Pred. No.: 106 Length: 1595  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 4 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-461-325-17 (1-1595)

QY 1 ThrvAlGuaaPaAlaGlu 6  
Db 827 ACACATGATCACTGTC 810

## RESULT 13

US-09-328-352-1770/C  
Sequence 1770, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 1770  
LENGTH: 1650  
TYPE: DNA  
ORGANISM: Acinetobacter baumannii

US-09-328-352-1770

## Alignment Scores:

Pred. No.: 110 Length: 1650  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 4 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-328-352-1770 (1-1650)

QY 2 AlAcYsIlleThrvAlGlu 7  
Db 348 GCTTGATCAGCGTCGAG 331

## RESULT 14

US-09-252-991A-15074/C  
Sequence 15074, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 15074  
LENGTH: 1968

TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15074

## Alignment Scores:

Pred. No.:	127	Length:	1968
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.00%	Indels:	0
DB:	4	Gaps:	0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-252-991A-15074 (1-1968)

QY 4 11eThVaIGluaspala 9  
DB 1506 ATCACCCTGAGATGCC 1489

## RESULT 15

US-08-579-777A-1

Sequence 1, Application US/08579777A

Patent No. 5912153

GENERAL INFORMATION:

APPLICANT: Enderlin, Carol S.

TITLE OF INVENTION: Seltremnikoff, Claude P.

TITLE OF INVENTION: Inducible inhibition of fungal growth using the antisense

TITLE OF INVENTION: constructs deviated therefrom.

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Davis, Graham & Stubbs L.L.P.

STREET: 370 Seventeenth Street

CITY: Denver

STATE: Colorado

COUNTRY: U.S.A.

ZIP: 80201-0185

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/579,777A

FILING DATE: 28-DEC-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/155,004

FILING DATE: 18-NOV-1993

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303)892-7370

TELEFAX: (303)893-1379

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2585 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Neurospora crassa

STRAIN: wild-type 74-DR 23-1VA

DEVELOPMENTAL STAGE: Mycelial

IMMEDIATE SOURCE:

LIBRARY: lambda Zap CDNA

CLONE: gs-1

POSITION IN GENOME:

CHROMOSOME/SEGMENT: linkage group V

US-08-579-777A-1

## Alignment Scores:

Pred. No.: 161

Length:

2585

Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.00%	Indels:	0
DB:	2	Gaps:	0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-08-579-777A-1 (1-2585)

QY 5 ThVaIGluaspala 10  
DB 1697 ACAGTCGAAGACCGCAG 1714

Search completed: December 23, 2003, 12:40:52  
Job time : 76 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 23, 2003, 12:00:30 ; Search time 2486 Seconds  
(Without alignments)  
13.404 Million cell updates/sec

Title: US-09-745-763-36\_COPY\_231\_240  
Perfect score: 10  
Sequence: 1 TACTIVEDAB 10

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2211978 segs, 1666101734 residues  
Word size: 1

Total number of hits satisfying chosen parameters: 4410318

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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-Q=/cgn2\_1/USPTO.epool\_p/US09745763/runat\_23122003\_120025\_20145/apd\_query.fasta-1.199  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=olp2n.rmpb -MIMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo  
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=quality -THR MIN=1  
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MTLEN=0  
-MAXLEN=200000000 -USER=US09745763@cgn2\_1.1107@runat\_23122003\_120025\_20145  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARK TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-Fgapop=6 -Fgapext=7 -Ygapop=60 -Ygapext=60 -DELOP=6 -DELEX=7

Database : Published Applications NA:\*

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2:	/cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
10:	/cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
11:	/cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
12:	/cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
14:	/cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
15:	/cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
16:	/cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
17:	/cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*
18:	/cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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1	10	100.0	1134	11	US-09-984-271-95	Sequence 95, Appl
2	10	100.0	1851	9	US-09-745-763-35	Sequence 35, Appl
3	10	100.0	1863	11	US-09-984-271-28	Sequence 28, Appl
4	6	60.0	37	14	US-10-004-717-69	Sequence 69, Appl
5	6	60.0	61	13	US-10-231-452-23	Sequence 23, Appl
6	6	60.0	98	13	US-10-231-452-47	Sequence 47, Appl
7	6	60.0	297	10	US-09-974-300-3664	Sequence 3664, Ap
8	6	60.0	357	13	US-10-231-452-50	Sequence 50, Appl
9	6	60.0	357	13	US-10-231-452-52	Sequence 52, Appl
10	6	60.0	357	13	US-10-231-452-59	Sequence 59, Appl
11	6	60.0	357	13	US-10-231-452-60	Sequence 60, Appl
12	6	60.0	391	11	US-09-803-719-73	Sequence 73, Appl
13	6	60.0	456	9	US-09-864-761-1999	Sequence 1999, Ap
14	6	60.0	472	11	US-09-918-995-20434	Sequence 20434, A
15	6	60.0	524	10	US-09-867-701-4823	Sequence 4823, Ap
16	6	60.0	609	14	US-10-004-717-14	Sequence 14, Appl
17	6	60.0	612	13	US-10-296-540-4	Sequence 4, Appl
18	6	60.0	653	13	US-10-027-632-228744	Sequence 228744,
19	6	60.0	653	14	US-10-027-632-228744	Sequence 228744,
20	6	60.0	665	13	US-10-027-632-128774	Sequence 128774,
21	6	60.0	665	14	US-10-027-632-128774	Sequence 128774,
22	6	60.0	1194	10	US-09-974-300-1072	Sequence 1072, Ap
23	6	60.0	1299	9	US-09-815-242-7603	Sequence 7603, Ap
24	6	60.0	1489	15	US-10-137-036-125	Sequence 125, App
25	6	60.0	1574	13	US-10-027-632-86669	Sequence 86669, A
26	6	60.0	1574	14	US-10-027-632-86669	Sequence 86669, A
27	6	60.0	1595	15	US-10-012-542-17	Sequence 17, Appl
28	6	60.0	1830	9	US-09-815-242-4504	Sequence 4504, Ap
29	6	60.0	1857	9	US-09-815-242-8469	Sequence 8469, Ap
30	6	60.0	2344	13	US-09-814-353-19093	Sequence 8872, Ap
31	6	60.0	2477	10	US-09-822-830A-252	Sequence 19093, A
32	6	60.0	3302	13	US-09-946-290-13	Sequence 252, App
33	6	60.0	3308	10	US-09-771-161A-71	Sequence 13, Appl
34	6	60.0	4116	13	US-10-296-540-3	Sequence 71, Appl
35	6	60.0	4125	13	US-10-296-540-1	Sequence 3, Appl
36	6	60.0	4510	14	US-10-005-983-1	Sequence 1, Appl
37	6	60.0	4638	13	US-10-006-285-403	Sequence 403, App
38	6	60.0	4693	13	US-10-240-965-85	Sequence 85, Appl
39	6	60.0	5049	15	US-10-084-817-114	Sequence 174, App
40	6	60.0	5128	13	US-10-133-937-57	Sequence 57, Appl
41	6	60.0	5128	13	US-10-341-434-156	Sequence 156, App
42	6	60.0	6336	8	US-08-781-986A-219	Sequence 219, App
43	6	60.0	7042	10	US-09-876-667-1	Sequence 1, Appl
44	6	60.0	7042	12	US-10-441-281-24	Sequence 24, Appl
45	6	60.0	7042	12	US-10-441-281-24	

ALIGNMENTS

RESULT 1  
US-09-984-271-95  
Sequence 95, Application US/09984271  
Publication No. US20030040088A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 71 Human Secreted Proteins  
FILE REFERENCE: PZ030P1  
CURRENT APPLICATION NUMBER: US/09/984, 271  
CURRENT FILING DATE: 2001-10-29  
PRIOR APPLICATION NUMBER: 09/482, 273  
PRIOR FILING DATE: 2000-01-13  
PRIOR APPLICATION NUMBER: PCT/US99/15849  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: 60/092, 921  
PRIOR FILING DATE: 1998-07-15  
PRIOR APPLICATION NUMBER: 60/092, 922  
PRIOR FILING DATE: 1998-07-15  
PRIOR APPLICATION NUMBER: 60/092, 956  
PRIOR FILING DATE: 1998-07-15  
NUMBER OF SEQ ID NOS: 267  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 95  
LENGTH: 1134

TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-984-271-95

Alignment Scores:  
Pred. No.: 0.00641 Length: 1134  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-984-271-95 (1-1134)

OY 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
Db 61 ACAGCCTGTATTACGGTGGAGATGCAGAA 90

RESULT 2  
US-09-745-763-35  
Sequence 35, Application US/09745763  
Patent No. US20020065394A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
McCoy, John M.  
Lavallie, Edward R.  
Collins-Racie, Lisa A.  
Evans, Cheryl  
Merberg, David  
Treacy, Maurice  
Spaulding, Vikki  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
ENCODING THEM  
NUMBER OF SEQUENCES: 219  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
City: Cambridge  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/745, 763  
FILING DATE: 18-Jun-2000  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne A.  
REGISTRATION NUMBER: 41,323  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1851 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-745-763-35

Alignment Scores:  
Pred. No.: 0.00984 Length: 1851  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 9

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-745-763-35 (1-1851)

OY 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
Db 789 ACAGCCTGTATTACGGTGGAGATGCAGAA 818

RESULT 3  
US-09-984-271-28  
Sequence 28, Application US/09984271  
Publication No. US20030040088A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 71 Human Secreted Proteins  
FILE REFERENCE: P2030P1  
CURRENT APPLICATION NUMBER: US/09/984, 271  
CURRENT FILING DATE: 2001-10-29  
PRIOR APPLICATION NUMBER: 09/482, 273  
PRIOR FILING DATE: 2000-01-13  
PRIOR APPLICATION NUMBER: PCT/US99/15849  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: 60/092, 921  
PRIOR FILING DATE: 1998-07-15  
PRIOR APPLICATION NUMBER: 60/092, 922  
PRIOR FILING DATE: 1998-07-15  
PRIOR APPLICATION NUMBER: 60/092, 956  
PRIOR FILING DATE: 1998-07-15  
NUMBER OF SEQ ID NOS: 267  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 28  
LENGTH: 1863  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-984-271-28

Alignment Scores:  
Pred. No.: 0.0099 Length: 1863  
Score: 10.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 11

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-984-271-28 (1-1863)

OY 1 ThrAlaCysIleThrValGluAspAlaGlu 10  
Db 789 ACAGCCTGTATTACGGTGGAGATGCAGAA 818

RESULT 4  
US-10-004-717-69/c  
Sequence 69, Application US/10004717  
Publication No. US20020192665A1  
GENERAL INFORMATION:  
APPLICANT: ZOCHBI, HUDA Y.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN  
ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,  
OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION  
FILE REFERENCE: P01899US4  
CURRENT APPLICATION NUMBER: US/10/004, 717  
CURRENT FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: 09/585, 645  
PRIOR FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: 60/176, 993  
PRIOR FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: 60/137, 060  
PRIOR FILING DATE: 1999-06-01  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 69  
LENGTH: 37  
TYPE: DNA

ORGANISM: Homo sapiens  
US-10-004-717-69

Alignment Scores:

Pred. No.:	13.5	Length:	37
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.00%	Indels:	0
DB:	14	Gaps:	0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-10-004-717-69 (1-37)

Qy 1 ThrlaCysleThral 6  
Db 27 ACGGATGCTACTGTC 10

RESULT 5  
US-10-231-452-23  
; Sequence 23, Application US/10231452  
; Publication No. US20030175273A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITTARA, KENYA  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: HOSAKA, EMI  
; APPLICANT: TANAKA, AKIKO  
; APPLICANT: KOIKE, MASAMICHI  
; TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF  
; FILE REFERENCE: 249-273  
; CURRENT APPLICATION NUMBER: US/10/231,452  
; CURRENT FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: JP 2001-265144  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 61  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-10-231-452-23

Alignment Scores:

Pred. No.:	20.9	Length:	61
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.00%	Indels:	0
DB:	13	Gaps:	0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-10-231-452-23 (1-61)

Qy 3 CysleThralGluasp 8  
Db 44 TGTATTCTGTGAGAGAC 61

RESULT 6  
US-10-231-452-47  
; Sequence 47, Application US/10231452  
; Publication No. US20030175273A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITTARA, KENYA  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: HOSAKA, EMI  
; APPLICANT: TANAKA, AKIKO  
; APPLICANT: KOIKE, MASAMICHI  
; TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF  
; FILE REFERENCE: 249-273  
; CURRENT APPLICATION NUMBER: US/10/231,452  
; CURRENT FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: JP 2001-265144  
; PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 98  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-10-231-452-47

Alignment Scores:

Pred. No.:	31.7	Length:	98
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.00%	Indels:	0
DB:	13	Gaps:	0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-10-231-452-47 (1-98)

Qy 3 CysleThralGluasp 8  
Db 61 TGTATTCTGTGAGAGAC 78

RESULT 7  
US-09-974-300-3664  
; Sequence 3664, Application US/09974300  
; Patent No. US20020146721A1  
; GENERAL INFORMATION:  
; APPLICANT: Berka, Randy M.  
; APPLICANT: Clausen, Ib Groth  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: 10085-500-US  
; CURRENT APPLICATION NUMBER: US/09/974,300  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/680,598  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/279,526  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 8481  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3664  
; LENGTH: 297  
; TYPE: DNA  
; ORGANISM: Bacillus licheniformis  
US-09-974-300-3664

Alignment Scores:

Pred. No.:	83.7	Length:	297
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.00%	Indels:	0
DB:	10	Gaps:	0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-974-300-3664 (1-297)

Qy 5 ThralGluaspAlaglu 10  
Db 74 ACTGTGAGAGAGCGCTGAG 91

RESULT 8  
US-10-231-452-50  
; Sequence 50, Application US/10231452  
; Publication No. US20030175273A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITTARA, KENYA  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: HOSAKA, EMI  
; APPLICANT: TANAKA, AKIKO  
; APPLICANT: KOIKE, MASAMICHI  
; TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF

FILE REFERENCE: 249-273  
CURRENT APPLICATION NUMBER: US/10/231,452  
CURRENT FILING DATE: 2003-04-18  
PRIOR APPLICATION NUMBER: JP 2001-265144  
PRIOR FILING DATE: 2001-08-31  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 50  
LENGTH: 357  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(357)  
US-10-231-452-50

Alignment Scores:  
Pred. No.: 98.4 Length: 357  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 13 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-10-231-452-50 (1-357)

QY 3 Cys11eThrValGluAsp 8  
|||  
278 TGTATTACTGTGGAAGAC 295

RESULT 9  
US-10-231-452-52  
Sequence 52, Application US/10231452  
Publication No. US20030175273A1  
GENERAL INFORMATION:  
APPLICANT: SHITTARA, KENYA  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: HOSAKA, EMI  
APPLICANT: TANAKA, AKIKO  
APPLICANT: KOIKE, MASAMICHI  
TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF  
FILE REFERENCE: 249-273  
CURRENT APPLICATION NUMBER: US/10/231,452  
CURRENT FILING DATE: 2003-04-18  
PRIOR APPLICATION NUMBER: JP 2001-265144  
PRIOR FILING DATE: 2001-08-31  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 52  
LENGTH: 357  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(357)  
US-10-231-452-52

Alignment Scores:  
Pred. No.: 98.4 Length: 357  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 13 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-10-231-452-52 (1-357)

QY 3 Cys11eThrValGluAsp 8  
|||  
278 TGTATTACTGTGGAAGAC 295

Db 278 TGTATTACTGTGGAAGAC 295

RESULT 10  
US-10-231-452-59  
Sequence 59, Application US/10231452  
Publication No. US20030175273A1  
GENERAL INFORMATION:  
APPLICANT: SHITTARA, KENYA  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: HOSAKA, EMI  
APPLICANT: TANAKA, AKIKO  
APPLICANT: KOIKE, MASAMICHI  
TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF  
FILE REFERENCE: 249-273  
CURRENT APPLICATION NUMBER: US/10/231,452  
CURRENT FILING DATE: 2003-04-18  
PRIOR APPLICATION NUMBER: JP 2001-265144  
PRIOR FILING DATE: 2001-08-31  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 59  
LENGTH: 357  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(357)  
US-10-231-452-59

Alignment Scores:  
Pred. No.: 98.4 Length: 357  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 13 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-10-231-452-59 (1-357)

QY 3 Cys11eThrValGluAsp 8  
|||  
278 TGTATTACTGTGGAAGAC 295

RESULT 11  
US-10-231-452-60  
Sequence 60, Application US/10231452  
Publication No. US20030175273A1  
GENERAL INFORMATION:  
APPLICANT: SHITTARA, KENYA  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: HOSAKA, EMI  
APPLICANT: TANAKA, AKIKO  
APPLICANT: KOIKE, MASAMICHI  
TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF  
FILE REFERENCE: 249-273  
CURRENT APPLICATION NUMBER: US/10/231,452  
CURRENT FILING DATE: 2003-04-18  
PRIOR APPLICATION NUMBER: JP 2001-265144  
PRIOR FILING DATE: 2001-08-31  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 60  
LENGTH: 357  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(357)  
US-10-231-452-60

## Alignment Scores:

Pred. No.: 98.4 Length: 357  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 13 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-10-231-452-60 (1-357)

QY 3 Cys11eThryValGuap 8

Db 278 TGTATCTACTGTGAAGAC 295

## RESULT 12

US-09-803-719-73/c

; Sequence 73, Application US/09803719  
; Publication No. US20030044783A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Lewis T.  
; APPLICANT: Escobedo, Jaime  
; APPLICANT: Innis, Michael A.  
; APPLICANT: Garcia, Pablo Dominguez  
; APPLICANT: Sudduth-Klinger, Julie  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Glese, Klaus  
; APPLICANT: Randazzo, Filippo  
; APPLICANT: Kennedy, Giulia C.  
; APPLICANT: Pot, David  
; APPLICANT: Kaasam, Altaf  
; APPLICANT: Lamsom, George  
; APPLICANT: Drmanac, Radoje  
; APPLICANT: Ckvenjakov, Radomir  
; APPLICANT: Dickson, Mark  
; APPLICANT: Drmanac, Snezana  
; APPLICANT: Labat, Ivan  
; APPLICANT: Leshkowitz, Dena  
; APPLICANT: Kita, David  
; APPLICANT: Garcia, Veronica  
; APPLICANT: Jones, Lee William  
; APPLICANT: Stache-Crain, Birgit  
; TITLE OF INVENTION: Human Genes and Gene Products  
; FILE REFERENCE: 1624.002  
; CURRENT APPLICATION NUMBER: US/09/803,719  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,609  
; NUMBER OF SEQ ID NOS: 2396  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 73  
; LENGTH: 391  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-803-719-73

## Alignment Scores:

Pred. No.: 107 Length: 391  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 11 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-803-719-73 (1-391)

QY 1 Thr1a1Cys11eThryVal 6

Db 218 ACAGCTTGACATCTGTC 201

## RESULT 13

US-09-864-761-1999

; Sequence 1999, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecmca-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 1999  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AP000403.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5

US-09-864-761-1999

## Alignment Scores:

Pred. No.: 122 Length: 456  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 9 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-864-761-1999 (1-456)

Oy 1 ThrValGluAspAlaGlu 6

Db 176 ACAGCTCGAGATGCTGAG 193

## RESULT 14

US-09-918-995-20434/C  
; Sequence 20434, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918, 995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235, 076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20434  
; LENGTH: 472  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(472)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-20434

## Alignment Scores:

Pred. No.: 126 Length: 472  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0  
DB: 11 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-918-995-20434 (1-472)

Oy 5 ThrValGluAspAlaGlu 10

Db 302 ACTGTCGAGATGCTGAG 285

## RESULT 15

US-09-867-701-4823/C  
; Sequence 4823, Application US/09867701  
; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Agiate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867, 701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4823  
; LENGTH: 524  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-867-701-4823

## Alignment Scores:

Pred. No.: 138 Length: 524  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.00% Indels: 0

DB: 10 Gaps: 0

US-09-745-763-36\_COPY\_231\_240 (1-10) x US-09-867-701-4823 (1-524)

Oy 5 ThrValGluAspAlaGlu 10

Db 144 ACTGTCGAGATGCTGAG 127

Search completed: December 23, 2003, 13:47:21  
Job time: 2487 secs